

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 14, 2003, 18:06:36 ; Search time 47 Seconds

(without alignments)
2134.366 Million cell updates/sec

Title: US-10-040-906a-2

Sequence: 1 MNVYNNNGRTTTCAYVVA.....GTQPELNNIMFVPTLPPY 632

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
A. Geneseq 19Jun03 :
1: /SIDS1/gcgdata/geneeq/geneeq-emb1/AA1980.DAT.*
2: /SIDS1/gcgdata/geneeq/geneeq-emb1/AA1981.DAT.*
3: /SIDS1/gcgdata/geneeq/geneeq-emb1/AA1982.DAT.*
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22: /SIDS1/gcgdata/geneeq/geneeq-emb1/AA2001.DAT.*
23: /SIDS1/gcgdata/geneeq/geneeq-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneeq/geneeq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3314	100.0	632	AAU02021	B. thuringiensis t
2	3048.5	92.0	633	AAW56966	CryIIA insecticida
3	3046.5	91.9	635	AAU02043	B. thuringiensis t
4	3043.5	91.8	634	AAW94259	CryIAb delta-endoc
5	3015.5	91.0	635	AAW57772	Amino acid sequenc
6	3010.5	90.8	633	AAW94260	CryIAb delta-endoc
7	3005.5	90.7	634	AAW94254	CryIAb delta-endoc
8	2974.5	89.8	633	AAW20030	Bacillus thuringie
9	2914.5	87.9	633	AAW57775	Amino acid sequenc

10	2913.5	87.9	633	AAW57774	Amino acid sequenc
11	2610.5	78.8	623	AAW57773	Amino acid sequenc
12	2582.5	77.9	625	AAU02044	B. thuringiensis t
13	1274.5	38.5	290	AAW3002	Sequence of P-2 pr
14	1082	32.6	706	AAW31199	Bacillus popilliae
15	499	15.1	99	AAW1356	Sequence of frame
16	336.5	10.2	643	AAW91462	67-kD protein toxi
17	336.5	10.2	643	AAW97735	B. thuringiensis t
18	331.5	10.0	710	AAU02041	Insecticidal prote
19	327.5	9.9	719	AAW66908	Insecticidal prote
20	327.5	9.9	719	AAW66911	B. thuringiensis t
21	325.5	9.8	719	AAW66910	Insecticidal prote
22	325	9.8	718	AAW66907	Insecticidal prote
23	325	9.8	719	AAW07073	Bacillus thuringie
24	324.5	9.8	719	AAW08041	81 kD endotoxin de
25	324.5	9.8	719	AAU02095	Bacillus thuringie
26	324.5	9.8	719	AAW66909	Insecticidal prote
27	314.5	9.5	1217	AAU02092	Bacillus thuringie
28	311.5	9.4	1156	AAW46857	Insecticidal prote
29	311.5	9.4	1156	AAW24960	Bacillus thuringie
30	311.5	9.4	1156	AAU02034	Bacillus thuringie
31	311	9.4	1157	AAW84587	B. thuringiensis t
32	310.5	9.4	1157	AAW84593	Amino acid sequenc
33	310.5	9.4	1157	AAW66912	Amino acid sequenc
34	310	9.3	1157	AAW84580	Amino acid sequenc
35	309	9.3	1157	AAW84584	Amino acid sequenc
36	309	9.3	1157	AAW84590	Amino acid sequenc
37	308	9.3	1157	AAW84581	Amino acid sequenc
38	308	9.3	1157	AAW84583	Amino acid sequenc
39	308	9.3	1157	AAW84588	Amino acid sequenc
40	308	9.3	1157	AAW84589	Amino acid sequenc
41	308	9.3	1157	AAW84592	Amino acid sequenc
42	307	9.3	1157	AAW46225	Bacillus thuringie
43	307	9.3	1157	AAW46225	Insecticidal prote
44	307	9.3	1157	AAW84582	Amino acid sequenc
45	307	9.3	1157	AAW84586	Amino acid sequenc

ALIGNMENTS

RESULT 1
ID AAU02021 standard; Protein; 632 AA.

AAU02021;
29-AUG-2001 (first entry)

B. thuringiensis toxic crystal protein, CryET31.

Delta endotoxin; Lepidopteran-active; crystal protein; insecticide;
transgenic plant; corn; wheat; soybean; oat; cotton; rice; yx; sorghum;
sugarcane; tomato; tobacco; kapok; flax; potato; barley; turf grass;
pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub;
cactus; tree cell; gypsy moth; looper; tobacco budworm; spruce budworm;
cotton leaf perforator; CryET31.

Bacillus thuringiensis.

WO200119859-A2.

22-MAR-2001.

13-SEP-2000; 2000WO-US25361.

15-SEP-1999; 99US-0153995.

(MONS) MONSANTO CO.

Baum JA, Chu C, Donovan WP, Gilmer AJ, Rupar MJ,
WPI; 2001-281518/29.

DR N-PSDB; AAS02464.
 XX Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides
 PT and the polynucleotides that encode them, useful for increasing the
 PT insect resistance of plant -
 XX
 PS Claim 5; Page 102-103; 173pp; English.
 XX
 CC The sequence represents a B. thuringiensis Lepidopteran-active
 CC delta-endotoxin, crystal protein CryET31. The Lepidopteran-active B.
 CC thuringiensis delta-endotoxin polypeptides may be used as compositions
 CC that are applied to plant crops to protect them from insect damage. The
 CC polynucleotides may be used in the production of transgenic plants that
 CC express the insecticidal polypeptides and consequently have improved
 CC insect resistance compared to non-transformed plants. Monocotyledonous or
 CC dicotyledonous plants may be protected in this way, for example corn,
 CC wheat, soybean, oat, cotton, rice, rye, sorghum, sugarcane, tomato,
 CC tobacco, kapok, flax, potato, barley, turf grass, pasture grass, berry,
 CC fruit, legume, vegetable, ornamental plant, shrub, cactus and/or tree
 CC cell. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm,
 CC cotton leaf perforator and spruce budworm) may be affected by application
 CC of the insecticidal polypeptides (full details given in specification).
 XX
 XX Sequence 632 AA:
 Query Match 100.0%; Score 3314; DB 22; Length 632;
 - Best Local Similarity 100.0%; Pred. No. 3.7e-259; Indels 0; Gaps 0;
 Matches 632; Conservative 0; Mismatches 0;
 QY 1 MNNVLANGRFTTICDANVVAADPPSPFEHKSIDTIRKEMEMKRTDHSIYVAIPVGVTSF 60
 SB 1 MNNVLANGRFTTICDANVVAADPPSPFEHKSIDTIRKEMEMKRTDHSIYVAIPVGVTSF 60
 QY 61 LKKVGSILGKRIISLWGLIPSGSTNLMODILRETEOFINRLNTDTLARVAELEG 120
 DB 61 LKKVGSILGKRIISLWGLIPSGSTNLMODILRETEOFINRLNTDTLARVAELEG 120
 QY 121 QANIRENOQVDFNLPONVPLSTSSVNTMOQLFLNRLPQFRVGVQVOLLPLPRAQ 180
 DB 121 QANIRENOQVDFNLPONVPLSTSSVNTMOQLFLNRLPQFRVGVQVOLLPLPRAQ 180
 QY 181 ANMHLSIRRVVYLNADENGISAATLRTYONVLYKNTTEYSNCINTYQTAFFGLNTRLHD 240
 DB 181 ANMHLSIRRVVYLNADENGISAATLRTYONVLYKNTTEYSNCINTYQTAFFGLNTRLHD 240
 QY 241 MLEFRTYVFLNFEVYSIWSLFTKYQSLVSSGANLYASGSGPQOTSFISQDMPFLYSLF 300
 DB 241 MLEFRTYVFLNFEVYSIWSLFTKYQSLVSSGANLYASGSGPQOTSFISQDMPFLYSLF 300
 QY 301 QVNSVYVINGSGARLTOTFFPIGIGLPGTTTHALLAAVYVSGVSSGPIGAVNPNFNS 360
 DB 301 QVNSVYVINGSGARLTOTFFPIGIGLPGTTTHALLAAVYVSGVSSGPIGAVNPNFNS 360
 QY 361 CSTFLPPLLPFVRSWLDGSDRGVNTVNTMOTESFESTGLRCGAFIARGNSNFPDY 420
 DB 361 CSTFLPPLLPFVRSWLDGSDRGVNTVNTMOTESFESTGLRCGAFIARGNSNFPDY 420
 QY 421 FTRNISGVPLVVRNEDLRPLAYNEIRNISPSGTGGLRAYMSVYNRQNTYAVHENG 480
 DB 421 FTRNISGVPLVVRNEDLRPLAYNEIRNISPSGTGGLRAYMSVYNRQNTYAVHENG 480
 QY 481 TWIHLAPEDYGTFTISPIHATOVNNTQTFIISFKNGQSDIARFOSNTYARTTLKNGN 540
 DB 481 TWIHLAPEDYGTFTISPIHATOVNNTQTFIISFKNGQSDIARFOSNTYARTTLKNGN 540
 QY 541 SYNYLYRVSSLSGNSLT RVYTNNGRVYTAENVTTTNDGVNDGARFIDIMNGVAVSDNT 600
 DB 541 SYNYLYRVSSLSGNSLT RVYTNNGRVYTAENVTTTNDGVNDGARFIDIMNGVAVSDNT 600
 QY 601 NVPLDINTVNSGTQFELMNMVFNPLNPIY 632
 DB 601 NVPLDINTVNSGTQFELMNMVFNPLNPIY 632

RESUR 2
 AAR5696
 ID AAR5696 standard; Protein; 633 AA.
 XX
 AC AAR5696;
 XX
 DT 25-MAR-2003 (updated)
 DT 27-MAR-1995 (first entry)
 XX
 DE CryIIA insecticidal crystal protein.
 XX
 KW CryIIA, CryIIA, CryIIA, CryC, P-2; CryBI, insecticidal protein crystal;
 KW lepidoptera; environmental insecticide; Bacillus thuringiensis; toxic;
 KW probe; hybridisation.
 XX
 OS Bacillus thuringiensis.
 XX
 PN US5338544-A.
 PD 16-AUG-1994.
 XX
 XX 26-FEB-1993; 93US-0023736.
 XX
 XX 16-APR-1987; 87US-0039542.
 PR 11-JUL-1989; 89US-0379015.
 PR 28-AUG-1991; 91US-0751452.
 PR 26-FEB-1993; 93US-0023736.
 XX
 PA (ECOG-) ECOGEN INC.
 XX
 XX Donovan WP;
 XX
 XX WPI; 1994-263236/32.
 DR N-PSDB; AAO71025.
 XX
 PT New Cry IIB protein - obtd. from the cry II B gene in Bacillus
 PT thuringiensis var. Kurstaki, active against lepidopteran insects
 XX
 PS Example 2; Fig 2A-2C; 39pp; English.
 XX
 CC This sequence shows the amino acid sequence of CryIIA protein.
 CC The CryIIA gene was used as a probe to identify CryIIA related
 CC sequences, ie. CryIIB. CryIIB encodes an insecticidal crystal
 CC protein isolated from Bacillus thuringiensis var. Kurstaki. It
 CC produces crystal proteins during sporulation which are specifically
 CC toxic to certain orders and species of insects, esp. lepidoptera.
 CC CryIIB can be used in compositions used as environmentally acceptable
 CC insecticides. (See also AAR5697-8)
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC
 XX
 XX Sequence 633 AA;
 SO
 Query Match 92.0%; Score 3048.5; DB 15; Length 633;
 - Best Local Similarity 90.7%; Pred. No. 1.1e-237;
 Matches 574; Conservative 34; Mismatches 24; Indels 1; Gaps 1;
 QY 1 MNNVLANGRFTTICDANVVAADPPSPFEHKSIDTIRKEMEMKRTDHSIYVAIPVGVTSF 60
 DB 1 MNNVLANGRFTTICDANVVAADPPSPFEHKSIDTIRKEMEMKRTDHSIYVAIPVGVTSF 60
 QY 61 LKKVGSILGKRIISLWGLIPSGSTNLMODILRETEOFINRLNTDTLARVAELEG 120
 DB 61 LKKVGSILGKRIISLWGLIPSGSTNLMODILRETEOFINRLNTDTLARVAELEG 120
 QY 121 QANIRENOQVDFNLPONVPLSTSSVNTMOQLFLNRLPQFRVGVQVOLLPLPRAQ 180
 DB 121 QANIRENOQVDFNLPONVPLSTSSVNTMOQLFLNRLPQFRVGVQVOLLPLPRAQ 180
 QY 181 ANMHLSIRRVVYLNADENGISAATLRTYONVLYKNTTEYSNCINTYQTAFFGLNTRLHD 240
 DB 181 ANMHLSIRRVVYLNADENGISAATLRTYONVLYKNTTEYSNCINTYQTAFFGLNTRLHD 240

QY 241 MLEPRTMFLNFEVYSIWSLFXKQSLIVSSGANLYASGSGPOQTSFTSQDMPFLYSLF 300
 DB 241 MLEPRTMFLNFEVYSIWSLFXKQSLIVSSGANLYASGSGPOQTSFTSQDMPFLYSLF 300
 QY 301 QVNSNYVLNFGSGARLTOTFPNIGGLPGTTTHALLARVYVSGVSGSDIGAV-FN0NF 359
 DB 301 QVNSNYVLNFGSGARLTOTFPNIGGLPGTTTHALLARVYVSGVSGSDIGAV-FN0NF 359
 QY 360 SCSTPLPPLTPPVNSLDSGDRGVNTVNTQTESFESTLGLRCGAFYARNSNPPD 419
 DB 361 NSTVLPPLSTPFVNSLDSGDRGVNTVNTQTESFESTLGLRCGAFYARNSNPPD 420
 QY 420 YFIRNISGVPLVNRNEDLRPLNRIEIRNIESPGTSGGAYVNSVHRKKNYVAHEN 479
 DB 421 YFIRNISGVPLVNRNEDLRPLNRIEIRNIESPGTSGGAYVNSVHRKKNYVAHEN 480
 QY 480 GTMHLAPEDYTGFTISPIHATOVNNQRTFISEKFGQDSDIRFQSNNTTARVTLRGNG 539
 DB 481 GTMHLAPEDYTGFTISPIHATOVNNQRTFISEKFGQDSDIRFQSNNTTARVTLRGNG 540
 QY 540 NSVNLVLRVSLGNSGTIRVTINGRVYTAENVNTTNDGVNDGARFELDINNKNVVASDN 599
 DB 541 NSVNLVLRVSLGNSGTIRVTINGRVYTAENVNTTNDGVNDGARFELDINNKNVVASDN 600
 QY 600 TNPPLDINTFNSGTQFELANIMEVPTNLPPLY 632
 DB 601 TNPPLDINTFNSGTQFELANIMEVPTNLPPLY 633

RESULT 3
 AA02043
 ID AA02043 standard; Protein, 635 AA.
 AC AA02043;
 XX 29-AUG-2001 (first entry)
 DT XX
 DE B. thuringiensis toxic crystal protein, CryET72.
 KM Delta endotoxin; Lepidopteran-active; crystal protein; insecticide;
 KM transgenic plant; corn; wheat; soybean; oat; cotton; rice; rye; sorghum;
 KM sugarcane; tomato; tobacco; kapok; flax; potato; turf grass;
 KM pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub;
 KM cactus; tree cell; gypsy moth; looper; tobacco budworm; spruce budworm;
 KM cotton leaf perforator; CryET72.
 XX
 OS Bacillus thuringiensis.
 XX
 PN WO200119859-A2.
 XX
 XX 22-MAR-2001.
 PD 13-SEP-2000; 2000WO-US25361.
 PF 15-SEP-1999; 99US-0153995.
 PR (MONS) MONSANTO CO.
 PA Baum JA, Chu C, Donovan WP, Gilmer AJ, Rupar MJ;
 PI WPI; 2001-281518/29.
 DR N-PSDB; AA502486.
 XX
 XX Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides
 PT and the polynucleotides that encode them, useful for increasing the
 PT insect resistance of plant -
 CC Claim 5; Page 158-160; 173pp; English.
 XX
 CC The sequence represents a B. thuringiensis lepidopteran-active
 CC delta-endotoxin, crystal protein CryET72. The lepidopteran-active B.
 CC thuringiensis delta-endotoxin polypeptides may be used as compositions
 CC that are applied to plant crops to protect them from insect damage. The

CC polynucleotides may be used in the production of transgenic plants that
 CC express the insecticidal polypeptides and consequently have improved
 CC insect resistance compared to non-transformed plants. Monocotyledonous or
 CC dicotyledonous plants may be protected in this way, for example corn,
 CC wheat, soybean, oat, cotton, rice, rye, sorghum, sugarcane, tomato,
 CC tobacco, kapok, flax, potato, barley, turf grass, pasture grass, berry,
 CC fruit, legume, vegetable, ornamental plant, shrub, cactus and/or tree
 CC cell. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm,
 CC cotton leaf perforator and spruce budworm) may be affected by application
 CC of the insecticidal polypeptides (full details given in specification).
 XX

SO Sequence 635 AA;

Query Match 91.9%; Score 3046.5; DB 22; Length 635;

Best local similarity 90.9%; Pred. No. 1.6e-237;

Matches 577; Conservative 31; Mismatches 24; Indels 3; Gaps 2;

QY 1 MNNVLANGRRTTCDAYVNVVADHPFSEHKSIDTIRKEMEMRTHSIXYAPVTVSSF 60
 DB 1 MNNVLANGRRTTCDAYVNVVADHPFSEHKSIDTIRKEMEMRTHSIXYAPVTVSSF 60
 QY 61 LKKGSLIGRILSLHMGILPPSGSTLMODILRETEQFLNQLRNTDTLARKVNAIBEL 120
 DB 61 LKKGSLIGRILSLHMGILPPSGSTLMODILRETEQFLNQLRNTDTLARKVNAIBEL 120
 QY 121 QANIREFNOQVDNFINPTONPVLSTTSVNTMOQFLRLPOFVQGYLLPLPFAA 180
 DB 121 QANIREFNOQVDNFINPTONPVLSTTSVNTMOQFLRLPOFVQGYLLPLPFAA 180
 QY 181 ANHLSFTRDVLNADBGISAATRTYQNTLKNYTRYSNCTINTQYARGLNRLHD 240
 DB 181 ANHLSFTRDVLNADBGISAATRTYQNTLKNYTRYSNCTINTQYARGLNRLHD 240
 QY 241 MLEPRTMFLNFEVYSIWSLFXKQSLIVSSGANLYASGSGPOQTSFTSQDMPFLYSLF 300
 DB 241 MLEPRTMFLNFEVYSIWSLFXKQSLIVSSGANLYASGSGPOQTSFTSQDMPFLYSLF 300
 QY 301 QVNSNYVLNFGSGARLTOTFPNIGGLPGTTTHALLARVYVSGVSGSDIGAV-FN0NF 359
 DB 301 QVNSNYVLNFGSGARLTOTFPNIGGLPGTTTHALLARVYVSGVSGSDIGAV-FN0NF 359
 QY 360 SCSTPLPPLTPPVNSLDSGDRGVNTVNTQTESFESTLGLRCGAFYARNSNPPD 419
 DB 361 NSTVLPPLSTPFVNSLDSGDRGVNTVNTQTESFESTLGLRCGAFYARNSNPPD 420
 QY 418 PNYFIRNISGVPLVNRNEDLRPLNRIEIRNIESPGTSGGAYVNSVHRKKNYVAHEN 477
 DB 421 PNYFIRNISGVPLVNRNEDLRPLNRIEIRNIESPGTSGGAYVNSVHRKKNYVAHEN 480
 QY 478 ENGTMHLAPEDYTGFTISPIHATOVNNQRTFISEKFGQDSDIRFQSNNTTARVTLRG 537
 DB 481 ENGTMHLAPEDYTGFTISPIHATOVNNQRTFISEKFGQDSDIRFQSNNTTARVTLRG 540
 QY 538 NGSNYVLNFGSGARLTOTFPNIGGLPGTTTHALLARVYVSGVSGSDIGAV-FN0NF 597
 DB 541 NGSNYVLNFGSGARLTOTFPNIGGLPGTTTHALLARVYVSGVSGSDIGAV-FN0NF 600
 QY 598 DNTNVPDLINTFNSGTQFELANIMEVPTNLPPLY 632
 DB 601 DNTNVPDLINTFNSGTQFELANIMEVPTNLPPLY 633

RESULT 4
 AA94259
 ID AA94259 standard; Protein, 634 AA.
 AC AA94259;
 XX 28-JUL-2000 (first entry)
 DT XX
 DE Cry22a delta-endotoxin.
 XX Transgenic plant; insect resistance; cry22a delta-endotoxin; Coleopteran;

QY	KNVYLNAGRRITL	CDAYNVVADHPSPFHKSLDTLRKMMEMKRDHSLVYAPVGTYSF	60
Db	1	MANVYNSGRITTCANINVAHADPFSEHKSLDTLRKMMEMKRDHSLVYAPVGTYSF	60
QY	61	LLKTVSGSLGKRILISELWGLIPPSGSTIMODILRETFOLNORLATDYLARVNALEGL	120
Db	61	LLKTVSGSLGKRILISELWGLIPPSGSTIMODILRETFOLNORLATDYLARVNALEGL	120
QY	121	QANIRENQOVNPLNPNQPVPLSTSSVNTMOQLFNLRLPQPVQGYOLLPLPFAQA	180
Db	121	QANIRENQOVNPLNPNQPVPLSTSSVNTMOQLFNLRLPQPVQGYOLLPLPFAQA	180
QY	181	ANMELSPTRDVVLNADDEWGISAAATLETPTQNYLKNYTTESYNYCINYYQIAFRGLNTRLHD	240
Db	181	ANMELSPTRDVVLNADDEWGISAAATLETPTQNYLKNYTTESYNYCINYYQIAFRGLNTRLHD	240
QY	241	MLEPRTYMLNPFEEYYSIWSLFFKXOSLIVSSGANLYASGSGPOQTQSFSDMPFLYSLF	300
Db	241	MLEPRTYMLNPFEEYYSIWSLFFKXOSLIVSSGANLYASGSGPOQTQSFSDMPFLYSLF	300
QY	301	QVNSNYVLNGFSGARLITQTPPNIGLPGTTTTALAAVNSYSGVSSGIDIGAV-ENQNF	359
Db	301	QVNSNYVLNGFSGARLITQTPPNIGLPGTTTTALAAVNSYSGVSSGIDIGAV-ENQNF	359
QY	360	SCSFPLPPLITFFVSWMLDSDGSDRGVNTVNTMOTESPESSTLGLRCGA--FTARGSNYF	417
Db	361	NCSIVPLPPLSTFFVSWMLDSDGSDRGVNTVNTMOTESPESSTLGLRCGAFTARGSNYF	420
QY	418	PDYIRNISGVPLVVRNEDLRPLAYNEIRNIBESQGTGGLRAYWVSVNRKNNIYAVH	477
Db	421	PDYIRNISGVPLVVRNEDLRPLAYNEIRNIBESQGTGGLRAYWVSVNRKNNIYAVH	480
QY	478	ENGFMILAPEDYGTFTISPIHATQVNNQRTFTISEKFGQGDSLRFGSNTTAAYTLRG	537
Db	481	ENGFMILAPEDYGTFTISPIHATQVNNQRTFTISEKFGQGDSLRFGSNTTAAYTLRG	540
QY	538	DNTNVPLDINVTNFSNGTOFELAMINMFPVPTNLPRY	632
Db	601	DNTNVPLDINVTNFSNGTOFELAMINMFPVPTNLPRY	635
RESULT 6			
AA94260 ID AAY94260 standard; Protein: 633 AA.			
AC	AA94260;		
XX	28-JUL-2000 (first entry)		
DT	Cry2ab delta-endotoxin.		
DE	Transgenic plant; insect resistance; cry2ab delta-endotoxin; Coleopteran;		
KW	Lepidopteran; Dipteran; plastid transit peptide; prp; insecticidal;		
XX	plastid targeting peptide.		
OS	Bacillus thuringiensis.		
XX	MO2000026371-A1.		
EN	11-MAY-2000.		
PD	04-NOV-1999; 99MO-US26086.		
XX	04-NOV-1998; 98US-0186002.		
PR	(MONS) MONSANTO CO.		
XX	Corbin DR, Romano CP,		
PL			
XX			

[illegible]

Db 601 SDVPLDINVTLSNGTQFDLMNIMVPTNISPLY 633

RESULT 7
ID AAY94254 standard; Protein; 634 AA.

AC AAY94254;

DT 28-JUL-2000 (first entry)

DE Cry2Ab delta-endotoxin.

KW Transgenic plant; insect resistance; cry2Ab delta-endotoxin; Coleoptera;

KW Lepidoptera; Diptera; plasmid transgene; PTP; insecticidal;

OS plasmid targeting peptide.

PD Bacillus thuringiensis.

PF WO200026371-A1.

PD 11-MAY-2000.

PF 04-NOV-1999; 99WO-US26086.

PF 04-NOV-1998; 98US-0186002.

PA (MONG) MONSANTO CO.

PI Corbin DR, Romano CP;

DR WPI; 2000-376130/32.

DR N-PSDB; AAI5556.

PT New method of expressing insecticidal proteins in plants transformed

PT with a Bacillus thuringiensis delta-endotoxin encoding gene resulting

PT in effective control of susceptible target pests

PS Claim 14; Page 82-83; 104pp; English.

XX The present sequence is the Cry2Ab delta-endotoxin. Delta-endotoxins are
XX produced by Bacillus thuringiensis during sporulation. These proteins are
XX toxic to certain species of insect e.g. Lepidoptera and Coleoptera
XX larvae. An insect-resistant transgenic plant has been constructed which
XX contains the cry2Ab gene. The cry2Ab gene would be transferred into
XX plants via expression vectors, which subsequently allow high expression
XX of the cry2Ab gene. The present sequence lacks Dipteran inhibitory
XX activity. Protection may be attained against insects such as Ostrina
XX spp., Diatraea spp., Helicoverpa spp., and Spodoptera spp., in Zea mays;
XX Heliothis virescens, Helicoverpa spp., Pectinophora spp., in Gossypium
XX hirsutum; Anticarsa spp., Pseudoplusia spp., Epinotia spp., in Glycine
XX max; and Scirpophaga incertulas in Oryza sativa. Expression of the
XX cry2Ab gene by a plant cell produces a fusion protein comprising
XX an amino-terminal plasmid transgene peptide (PTP) covalently linked to the
XX delta-endotoxin. The fusion protein functions to localise the
XX delta-endotoxin to a subcellular organelle or compartment.

XX Sequence 634 AA;

Query Match 90.7%; Score 3005.5; DB 21; Length 634;
Best Local Similarity 89.7%; Pred. No. 3.3e-234;
Matches 567; Conservative 39; Mismatch 25; Indels 1; Gaps 1;

QY 2 NNVLNNGRTTCDAYNVVAHDPFSEHKSIDTRKEMWKRTHSLVYAPVGVSSFL 61

DB 3 NSVLNNGRTTCDAYNVVAHDPFSEHKSIDTRKEMWKRTHSLVYAPVGVSSFL 62

QY 62 LKKVSGILGRIISSEIMGLIPSGSTNMODIIRTECPINORLNTTTLARVAHELQ 121

DB 63 LKKVSGILGRIISSEIMGLIPSGSTNMODIIRTECPINORLNTTTLARVAHELQ 122

QY 122 ANIREFNOVDNPLNPTQNPVPLSTSSVNTMOQLPLNLPQFVQYQALLPLPQA 181

Db 123 ANVEERNRQVDNPLNPNRNVAPELSTSSVNTMOQLPLNLPQFVQYQALLPLPQA 182

QY 182 NMELSFIRQVYVANDENGISAATLRTYQVYKNTTYSVYNTYQVAFGLNTRLHM 241

DB 183 NLHLSPFRVILNADENGISAATLRTYQVYKNTTYSVYNTYQVAFGLNTRLHM 242

QY 242 LEFRTYVFLNVEEYVSIWSLPEKQSLVSSGANLYASGSGPQQTQSFTSODMPLYSLFQ 301

DB 243 LEFRTYVFLNVEEYVSIWSLPEKQSLVSSGANLYASGSGPQQTQSFTSODMPLYSLFQ 302

QY 302 VNSVYVNLNGSGARLSTQFPNIGLPGCTTHALLARVYSGVSSGDGA-VENQNS 360

DB 303 VNSVYVNLNGSGARLSTQFPNIGLPGCTTHALLARVYSGVSSGDGA-VENQNS 362

QY 361 CSTFLPPLLPVRSWLDSDGSDGVNTVYVNTWQTESFETLGRGAPFARQNSNYPDY 420

DB 363 CSTFLPPLLPVRSWLDSDGSDGVNTVYVNTWQTESFETLGRGAPFARQNSNYPDY 422

QY 421 FTRISGVEPLVYREDDLRPLAYNEIRNIESPSGTPGCLAAVYVSVHNRKNYAVHENG 480

DB 423 FTRISGVEPLVYREDDLRPLAYNEIRNIESPSGTPGCLAAVYVSVHNRKNYAVHENG 482

QY 481 TWIHLAPEDYGTFTISPIHATOVNNTQRTFISEKRGQDGLRFEQNTTARYTLRNGN 540

DB 483 SMHLAPNDYGTFTISPIHATOVNNTQRTFISEKRGQDGLRFEQNTTARYTLRNGN 542

QY 541 SYNLXLRVSSIGNSTIRVTNGVYVYASVNTTNNGVNDGARPLDINNANVVASDNT 600

DB 543 SYNLXLRVSSIGNSTIRVTNGVYVYASVNTTNNGVNDGARPLDINNANVVASDNT 602

QY 601 NVPLDINVTNSGTQFDLMNIMVPTNISPLY 632

DB 603 DVPLDINVTLSNGTQFDLMNIMVPTNISPLY 634

RESULT 8

ID AAR20030 standard; Protein; 633 AA.

AC AAR20030;

DT 07-APR-1992 (first entry)

DE Bacillus thuringiensis CryIIB crystal toxin.

KW B.t. crystal protein; insecticide; Lepidoptera; larva; corn earworm;

KW Heliothis zea.

OS Bacillus thuringiensis.

PN US5073632-A.

PD 17-DEC-1991.

PF 11-JUL-1989; 89US-0379015.

PR 11-JUL-1989; 89US-0379015.

PR 16-APR-1987; 87US-0039542.

PA (ECOG-) ECOGEN INC.

PI Donovan WP;

DR WPI; 1992-016224/02.

DR N-PSDB; AAO20202.

PT Bacillus thuringiensis cryIIB protein gene - used to obtain the

PT protein for use as an insecticidal cpd. against lepidopteran

PT insects

PS Disclosure; Fig 6; 30pp; English.

CC The cryIIb gene was isolated from a B.t. strain using the cryIIa
CC gene as probe. The cryIIb gene encodes a 613 amino acid protein of
CC calculated mol. wt. 70,749. The insecticidal toxin CryIIb is twice
CC as toxic as the CryIIa protein against the lepidopteran *Heliothis*
CC zea.

SQ Sequence 633 AA;

Query Match	89.8%;	Score 2974.5;	DB 13;	Length 633;
Best Local Similarity	88.8%;	Pred. No. 1.1e-231;		
Matches 562;	Conservative 39;	Mismatches 31;	Indels 1;	Gaps 1

QY	1	MANVLANNGSTTTI	CAVAVNVVAHDPSPSEKHSIDLTIREKHEWKEKRTDHSIYALPVCYVSF	60
Db	1	MSVATNSGTTT	CDANVVAHDPSPFOKHSIDTVOKEWEMKKNHSIYDLPVGVVASF	60
QY	61	LKKVSGSLIGKRI	LSIEMWGLIPPSGSTMODILIRETOFLNORLNTDYLARVNAELGL	120
Db	61	LKKVSLIAGKRI	LSIEMRLIPPSGSTMODILIREKHEKFORLINTDYLARVNAELGJL	120
QY	121	QANIREFNOQVNF	PLNPTQNPVPLSTTSVNTMOQLFRLRPOQPVGOYQLLLPLFPOA	180
Db	121	QAVVEEKNQVNF	PLNPNRAVPLSTTSVNTMOQLFRLRPOQMGQQLLLPLFPOA	180
QY	181	ANMHSFETD	VDVLANDDEMGISAATLTQNTLKYTTYEYSNTCINTTQTAFCGLNTRLHD	240
Db	181	ANMHSFETD	VDVLANDDEMGISAATLTQNTLKYTTYEYSNTCINTTQTAFCGLNTRLHD	240
QY	241	MESEFTYME	LANFEVSIWGLFKYOSLIVSSGANLYASGSGOQTOSFTSODMPFLYSILF	300
Db	241	MESEFTYME	LANFEVSIWGLFKYOSLIVSSGANLYASGSGOQTOSTSODMPFLYSILF	300
QY	301	QVNSNVVLNG	SPGARLOTPEPNTIGLPCGTTTHALLAAVYVSGVSSGDTGA-VPNONF	360
Db	301	QVNSNVVLNA	SPKARLSNTPEPNTIYALPOSTITTHALLAAVYVSGVSSGDTGASPNONF	360
QY	360	SGCTETPL	LLTPPVASWLDGSDRGQVNTVNTMOTESFESTYLGRCAQAPFARNSNYPPD	419
Db	361	NCSTETPL	LLTPPVASWLDGSDRGQVNTVNTMOTESFESTYLGRCAQAPFARNSNYPPD	420
QY	420	YFNRNISG	VPVNEDELPPLHYNEINISPSGPGGLRAYVVSVAHNKNKIIVAHEN	479
Db	421	YFNRNISG	VPVNEDELPPLHYNEINISPSGPGGARINVSVAHNKNKIIVAHEN	480
QY	480	GTMIHIA	PEPTYGTTISPLHATOVNNQRTFISFKFGNGDLSLPEOSNTTARYYTLRANG	539
Db	481	GSMIHIAP	PEPTYATFISPLHATOVNNQRTFISFKFGNGDLSLPEOANTTARYYTLRANG	540
QY	540	NSVNLILAR	VSIGSTRIVINGRAYVTSANVTNTNDDVDNNGARPLDINNNGVVAADN	599
Db	541	NSVNLILAR	VSIGSTRIVINGRAYTANVTNTNDDVDNNGARPSDINQNVVAASN	600
QY	600	TNYPLDINT	NSGOFELMIMFVPTLPIY	632
Db	601	SDVPLDINT	NSGOFELMIMFVPTNISPLY	633

RESULT 9
AAW75775
ID AAW75775 standard; Protein; 633 AA

AC	AAW75775;
XX	
DT	02-DEC-1998 (first entry)

Amino acid sequence of Lepidoteran-active 86I2 toxin.

KM 8612 toxin; PCR; primer; amplification; *Bacillus thuringiensis*; probe
KM lepidoptera; pest; pesticide; *Ostrinia nubilalis*; *Heliothis virescens*;
KM *Helicoverpa zea*; hybridisation.

OS *Bacillus thuringiensis.*
XX

PN	WO9840490-A1.
XX	
PD	17-SEP-1998.
XX	
PF	13-MAR-1998;
XX	98WO-US05081
PR	13-MAR-1997;
XX	97US-0040512

PT New insecticidal *Bacillus thuringiensis* toxins - useful for
PT controlling lepidopteran pests, especially *Ostrinia nubilalis*,
PT *Heliothis virescens* and *Helicoverpa zea*
XX

PS Claim 5; Pages 36-38; 50pp; English
 vx

This is the amino acid sequence of a novel *Bacillus thuringiensis* toxin used in the method of the invention, to control lepidopteran pests. The new toxins are useful as pesticides, especially for the control of *Ostrinia nubilalis*, *Heliothis virescens*, and *Helicoverpa zea*. The polynucleotide coding sequences are useful for recombinant expression of the toxins and the primers, together with probes derived from the new sequences, are useful for the identification and characterisation of novel genes that encode pesticidal toxins.

50 Sequence 633 AA

Query Match	87.9%;	Score 2914.5;	DB 19;	Length 633;
Best Local Similarity	87.0%;	Pred. No. 7.6e-227;		
Matches 551; Conservative	44;	Mismatches 37;	Indels 1;	Gaps 1;

Qy	1	NNVNLNNGEITICDANYVNVHDPBSFEHKSJDTITREKMEKMRDSDHSLYAPVGVYSSF	60
Dp	1	NNVNLNNGNNTICDANYVNVHDPBSFQHSKSDJTIQKEMEMKONHSLYDPIVGVYASF	60
Qy	61	LAKVSSLIGRRILSELNGLIPPSGSSTLMMODILARETQFOFLNORLNDTLARVNAELRGL	120
Dp	61	LKKKGSLLIGRRILSELNRLIPPSGSSTLMEDILARETBKFLNQLKNTDLSRNMELTGL	120
Qy	121	QANIEFNOQDNDLNFQNPVPLSTISSVYVMOQLFLARLPQRVGICYLLPLPFOA	180
Dp	121	QANVEFNRQDNDLNFNRNAVPLSTISSVYVMOQLFLNRLSOFOMQGYOLLPLPFOA	180
Qy	181	ANHELSEFRDVLNAEBWGISAAATLRTQYVLYKQNYTTERSYNCYNTQZAFRGLNTRLHD	240
Dp	181	ANHLSEYRDVLNAEBWGISAAATLRTQYHNLNTRYDSNYCIDTYQZAFRGLNTRLHD	240
Qy	241	MEFRTYVPLNVEPYVISIMSLFKYOSLLSSGANLYASGSPQOOTSFPISQDMPPLSYLF	300
Dp	241	MEFRTYVPLNVEPYVISIMSLFKYOSLLSSGANLYASGSGQOOTSFPISQDMPPLSYLF	300
Qy	301	QVNSVYLVNGSGARLTQTFPNIIGGLPQITTTTHALLAARVYSGVSSGDI-GAVFNQNF	358
Dp	301	QVNSVYLVNGSGARLFTTFPNIIGGLPQSTTTQALLAARVYSGGISGSSFNQNF	360
Qy	360	SGSTFPLPLPPFVRKAMLSGSDRGVNYTVMQTESPEPTLGLRCGAPFAAGSNVPEPD	419
Dp	361	NCKTISPEPLSTFVRKAMLSGSDRGVNYTVMQTESPEPTTSGLRCAFPKSNVNPYG	420
Qy	420	YFIRNISGAVPLVWNEDLRRPLAHNEIRNISPSGTPGGLAIVYVSVHNRKNNIYAVHEN	479
Dp	421	YFIRNISGAVSLVRNEDLRRPLAYNERKNIESPSGPGGAAYVSVHNRKNNIYAVHEN	480
Qy	480	GTMILHAPEDYGTFTSPHATQVNNQTRFTISEKPKNGOGLSFPBOSNTMTRAYTLRNG	539
Dp	481	GTMILHAPEDYGTFTSPHATQVNNQTRFTISEKPKNGOGLSFPBOSNTMTRAYTLRNG	540
Qy	540	NSYNLYRVSLSGNTIRVTJLNGRVYTAASNVTNTNNQDVNDGARELDINNANVVASDN	599

DB 541 NSYNLYRVSSIGNSTIRVTINSGVYTAASNVTTTNDGNDNGAFSDINIGNVASSN 600
 QY 600 TNVPLDINVTNSGTOPELMANIMFVPTNLPPIY 632
 DB 601 SDVPLDINVTNLSGTQFDLMNIMLVPTNLSPLY 633

RESULT 10
 ID AAM75774 standard; Protein: 633 AA.
 AC AAM75774;
 XX 02-DEC-1998 (first entry)
 DT Amino acid sequence of lepidopteran-active HD525 toxin.
 XX
 DE HD525 toxin; PCR, primer; amplification; *Bacillus thuringiensis*; probe;
 KM lepidoptera; pest; pesticide; *Ostrinia nubilalis*; *Heliothis virescens*;
 KM *Helicoverpa zea*; hybridisation.
 XX
 OS *Bacillus thuringiensis*.
 XX MO9840490-A1.
 PN 17-SEP-1998.
 BD 13-MAR-1998; 98WO-US05081.
 XX 13-MAR-1997; 97US-0040512.
 PR 13-MAR-1997; 97US-0040512.
 XX 2X
 PA (MYCO) MYCOGEN CORP.
 XX
 PI Muller-Cohn J, Narva KE, Schnepf HE;
 XX WPI, 1998-506734/43.
 DR N-PSDB; AAV52611.
 XX
 PT New insecticidal *Bacillus thuringiensis* toxins - useful for
 PT controlling lepidopteran pests, especially *Ostrinia nubilalis*.
 PT *Heliothis virescens* and *Helicoverpa zea*
 PS Claim 14; Pages 32-34; 50pp; English.
 XX
 CC This is the amino acid sequence of a novel *Bacillus thuringiensis* toxin
 CC used in the method of the invention, to control lepidopteran pests.
 CC The new toxins are useful as pesticides, especially for the control of
 CC *Ostrinia nubilalis*, *Heliothis virescens*, and *Helicoverpa zea*. The
 CC polynucleotide coding sequences are useful for recombinant expression
 CC of the toxins and the primers, together with probes derived from the
 CC new sequences, are useful for the identification and characterisation
 CC of novel genes that encode pesticidal toxins.
 CC
 XX Sequence 633 AA;
 SO

Query Match 87.9%; Score 2913.5; DB 19; Length 633;
 Best Local Similarity 87.2%; Pred. No. 9,1e-227;
 Matches 552; Conservative 42; Mismatches 38; Indels 1; Gaps 1;

QY 1 MNNVTNNGRTTICDANNVADHPSPFHSKSLDTIRKEMWEMKRDHSDHVAPIVGTASSF 60
 DB 1 MNNVTNNGRTTICDANNVADHPSPFHSKSLDTIRKEMWEMKRDHSDHVAPIVGTASSF 60
 QY 61 LKRVGSLIGKRIISLWGLIFPSGSTNLMODILRETOFLOLNTLTTLARVNELEG 120
 DB 61 LKRVGSLIGKRIISLWGLIFPSGSTNLMODILRETOFLOLNTLTTLARVNELEG 120
 QY 121 QANIREPQOVNDPFLNPTONPVPLSTSSVNTMOULFNRLPORVGYOGLLLPLPFOA 180
 DB 121 QANIREPQOVNDPFLNPTONPVPLSTSSVNTMOULFNRLPORVGYOGLLLPLPFOA 180
 QY 181 ANMHLSPIRDVVLNADWEGISAATLRTYONLKNYTTESVNCYNTVQTAFRGLNTRLHD 240

DB 181 ANMHLSPIRDVVLNADWEGISAATLRTYONLKNYTTESVNCYNTVQTAFRGLNTRLHD 240
 QY 241 MEERTYVFNVEEYVSIWLFKQSLIVSSGANLYASGSGPOOTQSFSDWPFYSLF 300
 DB 241 MEERTYVFNVEEYVSIWLFKQSLIVSSGANLYASGSGPOOTQSFSDWPFYSLF 300
 QY 301 QVNSVYVANGFSGARLTOTFPNIGGLPGTTTHALLAARVWYSGVSSGDI -GAVFNQNF 359
 DB 301 QVNSVYVANGFSGARLTOTFPNIGGLPGTTTHALLAARVWYSGVSSGDI -GAVFNQNF 359
 QY 360 SCSTFLPPLLPFPVPSGWSLSDSGVGVVYVNTQTESFESTLGLRCGAFARANSYFED 419
 DB 360 SCSTFLPPLLPFPVPSGWSLSDSGVGVVYVNTQTESFESTLGLRCGAFARANSYFED 419
 QY 361 NCNTTSPPLSTSPFRIMDSGSDRGVYVNTQTESFESTLGLRCGAFARANSYFED 420
 DB 361 NCNTTSPPLSTSPFRIMDSGSDRGVYVNTQTESFESTLGLRCGAFARANSYFED 420
 QY 420 YFIRNIGSVPLVNRNEDLRPLAHNEIRNIESGTPGGLARVWYVYHKNKNTYAVHEN 479
 DB 420 YFIRNIGSVPLVNRNEDLRPLAHNEIRNIESGTPGGLARVWYVYHKNKNTYAVHEN 479
 QY 480 GTMHLAPEDYTGFTISPIHATQVNNQTRFISEKFGNQGSLRPEQSNNTAAYTLRGNG 539
 DB 480 GTMHLAPEDYTGFTISPIHATQVNNQTRFISEKFGNQGSLRPEQSNNTAAYTLRGNG 539
 QY 481 GTMHLAPEDYTGFTISPIHATQVNNQTRFISEKFGNQGSLRPEQSNNTAAYTLRGNG 540
 DB 481 GTMHLAPEDYTGFTISPIHATQVNNQTRFISEKFGNQGSLRPEQSNNTAAYTLRGNG 540
 QY 540 NSYNLYRVSSIGNSTIRVTINSGVYTAASNVTTTNDGNDNGAFSDINIGNVASSN 599
 DB 541 NSYNLYRVSSIGNSTIRVTINSGVYTAASNVTTTNDGNDNGAFSDINIGNVASSN 600
 QY 600 TNVPLDINVTNSGTOPELMANIMFVPTNLPPIY 632
 DB 601 SDVPLDINVTNLSGTQFDLMNIMLVPTNLSPLY 633

RESULT 11
 ID AAM75773 standard; Protein: 623 AA.
 AC AAM75773;
 XX 02-DEC-1998 (first entry)
 DT Amino acid sequence of lepidopteran-active HD573 toxin.
 XX
 DE HD573 toxin; PCR, primer; amplification; *Bacillus thuringiensis*; probe;
 KM lepidoptera; pest; pesticide; *Ostrinia nubilalis*; *Heliothis virescens*;
 KM *Helicoverpa zea*; hybridisation.
 XX
 OS *Bacillus thuringiensis*.
 XX MO9840490-A1.
 PN 17-SEP-1998.
 BD 13-MAR-1998; 98WO-US05081.
 XX 13-MAR-1997; 97US-0040512.
 PR 13-MAR-1997; 97US-0040512.
 XX
 PA (MYCO) MYCOGEN CORP.
 XX
 PI Muller-Cohn J, Narva KE, Schnepf HE;
 XX WPI, 1998-506734/43.
 DR N-PSDB; AAV52610.
 XX
 PT New insecticidal *Bacillus thuringiensis* toxins - useful for
 PT controlling lepidopteran pests, especially *Ostrinia nubilalis*,
 PT *Heliothis virescens* and *Helicoverpa zea*
 PS Claim 14; Pages 28-30; 50pp; English.
 XX
 CC This is the amino acid sequence of a novel *Bacillus thuringiensis* toxin
 CC used in the method of the invention, to control lepidopteran pests.
 CC The new toxins are useful as pesticides, especially for the control of
 CC *Ostrinia nubilalis*, *Heliothis virescens*, and *Helicoverpa zea*. The

CC polynucleotide coding sequences are useful for recombinant expression
 CC of the toxins and the primers, together with probes derived from the
 CC new sequences, are useful for the identification and characterisation
 CC of novel genes that encode pesticidal toxins.

XX Sequence 623 AA;

Query Match 78.8%; Score 2610.5; DB 19; Length 623;
 Best Local Similarity 80.3%; Pred. No. 2.9e-202;
 Matches 508; Conservative 46; Mismatches 68; Indels 11; Gaps 6;

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QY 1 MNNVANNRRTTICDANNVVAADPPSEFHSKSLDTTKEKMEKRTDLSLYVAVIGVTSF 60
DB 1 MNNVANNRRTTICDANNVVAADPPSEFHSKSLDTTKEKMEKRTDLSLYVAVIGVTSF 60
QY 61 LKKGVSILGKRIISELMGLIFPSGSTNIMODILRETEOFANORLNTDTLARVNALEGL 120
DB 61 LKKGVSILGKRIISELMGLIFPSGSTNIMODILRETEOFANORLNTDTLARVNALEGL 120
QY 121 QANIRENOOVNPNLPONVPLSTSSVNTMOQLFANLPQFRVQGLILPLPQA 180
DB 121 QANVAFNRQVNFNPNQVPLALIDSVNTLQQLLSLPLQGLQGLILPLPQA 180
QY 181 ANNELSFIRDVVLANDEMGISAATLRTYONLKNYTESNCTNTYOTAFRGINTRLHD 240
DB 181 ANNELSFIRDVVLANDEMGISAATLRTYONLKNYTESNCTNTYOTAFRGINTRLHD 240
QY 241 MEERTYMEFLNVEFVYSIMSLFKYOSLLVSSGANLYASGSGPQOTQTSODMPFLYSLF 300
DB 241 MEERTYMEFLNVEFVYSIMSLFKYOSLLVSSGANLYASGSGPQOTQTSODMPFLYSLF 300
QY 301 QVNSVYVNLGSGARLQTEPNIGLPGTTTHALLAARVNSGVSIGDYG-AVFNQNF 359
DB 299 QVNSVYVNLGSGARLQTEPNIGLPGTTTHALLAARVNSGVSIGDYG-AVFNQNF 358
QY 360 SCSTPLPLPLTFPVRSWLDGSGDRGVNTVMQTESFESTGLRCGAFYAKGNSVFPD 419
DB 359 NISTFENLPQTFPIRSWLDGSGDRGVNTVMQTESFESTGLRCGAFYAKGNSVFPD 417
QY 420 YFIRNISGVPLVWNEDELRRPLHYNEIRNISPSGTRCGILRAYMSVHNRYAVHEN 479
DB 418 YFIRNISGVPLVWNEDELRRPLHYNEIRNISPSGTRCGILRAYMSVHNRYAVHEN 471
QY 480 GIMHILAPEDYTGTTSPFHAQVNNQTRFISEKFGNODSLRPEOSNTTAYTLRNG 539
DB 472 GIMHILAPEDYTGTTSPFHAQVNNQTRFISEKFGNODSLRPEOSNTTAYTLRNG 531
QY 540 NSYNLYKVSLSGSTRITNGRYTASVNTTNDGNNNGARFELDIKMGVYASDN 599
DB 532 NSYNLYKVSLSGSTRITNGRYTASVNTTNDGNNNGARFELDIKMGVYASDN 590
QY 600 TWEPLDINTVFNSTGPELMTIMPVFNPLPIY 632
DB 591 TWEPLDINTVFNSTGPELMTIMPVFNPLPIY 623

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RESULT 12

AAU02044 standard; Protein; 625 AA.

AAU02044; 29-AUG-2001 (first entry)

B. thuringiensis toxic crystal protein, CryET73.

XX Delta endotoxin; Lepidopteran-active; crystal protein; insecticide;
 KW transgenic plant; corn; wheat; soybean; oat; cotton; rice; rye; sorghum;
 KW sugarcane; tomato; tobacco; kapok; flax; potato; barley; turf grass;
 KW pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub;
 KW cactus; tree cell; gypsy moth; looper; tobacco budworm; spruce budworm;
 KW cotton leaf perforator; CryET73.

OS Bacillus thuringiensis.

XX W0200119959-A2.

XX 22-MAR-2001.

XX 13-SEP-2000; 2000MO-US25361.

XX 15-SEP-1999; 99US-0153995.

XX (MONS) MONSANTO CO.

XX Baum JA, Chu C, Donovan WP, Gilmer MJ, Rupar MJ;

XX WPI; 2001-281518/29.

XX N-PSDB; AAS02487.

XX Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides
 PT and the polynucleotides that encode them, useful for increasing the
 XX insect resistance of plant -

XX Claim 5; Page 163-164; 173pp; English.

The sequence represents a B. thuringiensis lepidopteran-active
 CC delta-endotoxin, crystal protein CryET73. The lepidopteran-active B.
 CC thuringiensis delta-endotoxin polypeptides may be used as compositions
 CC that are applied to plant crops to protect them from insect damage. The
 CC polynucleotides may be used in the production of transgenic plants that
 CC express the insecticidal polypeptides and consequently have improved
 CC insect resistance compared to non-transformed plants. Monocotyledonous or
 CC dicotyledonous plants may be protected in this way, for example corn,
 CC wheat, soybean, oat, cotton, rice, rye, sorghum, sugarcane, tomato,
 CC tobacco, kapok, flax, potato, barley, turf grass, pasture grass, berry,
 CC fruit, legume, vegetable, ornamental plant, shrub, cactus and/or tree
 CC cell. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm,
 CC cotton leaf perforator and spruce budworm) may be affected by application
 CC of the insecticidal polypeptides (full details given in specification).

XX Sequence 625 AA;

Query Match 77.9%; Score 2582.5; DB 22; Length 625;
 Best Local Similarity 80.7%; Pred. No. 5.3e-200;
 Matches 503; Conservative 44; Mismatches 65; Indels 11; Gaps 6;

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QY 1 MNNVANNRRTTICDANNVVAADPPSEFHSKSLDTTKEKMEKRTDLSLYVAVIGVTSF 60
DB 1 MNNVANNRRTTICDANNVVAADPPSEFHSKSLDTTKEKMEKRTDLSLYVAVIGVTSF 60
QY 61 LKKGVSILGKRIISELMGLIFPSGSTNIMODILRETEOFANORLNTDTLARVNALEGL 120
DB 61 LKKGVSILGKRIISELMGLIFPSGSTNIMODILRETEOFANORLNTDTLARVNALEGL 120
QY 121 QANIRENOOVNPNLPONVPLSTSSVNTMOQLFANLPQFRVQGLILPLPQA 180
DB 121 QANVAFNRQVNFNPNQVPLALIDSVNTLQQLLSLPLQGLQGLILPLPQA 180
QY 181 ANNELSFIRDVVLANDEMGISAATLRTYONLKNYTESNCTNTYOTAFRGINTRLHD 240
DB 181 ANNELSFIRDVVLANDEMGISAATLRTYONLKNYTESNCTNTYOTAFRGINTRLHD 240
QY 241 MEERTYMEFLNVEFVYSIMSLFKYOSLLVSSGANLYASGSGPQOTQTSODMPFLYSLF 300
DB 241 MEERTYMEFLNVEFVYSIMSLFKYOSLLVSSGANLYASGSGPQOTQTSODMPFLYSLF 300
QY 301 QVNSVYVNLGSGARLQTEPNIGLPGTTTHALLAARVNSGVSIGDYG-AVFNQNF 359
DB 299 QVNSVYVNLGSGARLQTEPNIGLPGTTTHALLAARVNSGVSIGDYG-AVFNQNF 358
QY 360 SCSTPLPLPLTFPVRSWLDGSGDRGVNTVMQTESFESTGLRCGAFYAKGNSVFPD 419
DB 359 NISTFENLPQTFPIRSWLDGSGDRGVNTVMQTESFESTGLRCGAFYAKGNSVFPD 417
QY 420 YFIRNISGVPLVWNEDELRRPLHYNEIRNISPSGTRCGILRAYMSVHNRYAVHEN 479

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DB 418 YFRINISGVVGTISNADLAPLAFENIRDI---GTTA--VSLVTVNRRKNNTYDTHEN 471
 QY 480 GTMHLAPEDYTGFTISPIHATOVNQTPTFISEKFGNQGDSLRFEGSNTTARYTLRGNG 539
 DB 472 GTMHLAPEDYTGFTISPIHATOVNQTPTFISEKFGNQGDSLRFELSNNTARYTLRGNG 531
 QY 540 NSNTLYRVSLGNSITRTVNTNRRVYTSANVTNTNDGVNDGAFPLDIMGVYASDN 599
 DB 532 NSNTLYRVSLGNSITRTVNTNRRVYTSANVTNTNDGVNDGAFPLDIMGVYASDN 590
 QY 600 TNPVLDINTVENSCTOFELANMIM 622
 DB 591 TNPVLDIQVTENDNPQFELANMIM 613

RESULT 13
 AAP83002
 ID AAP83002 standard; protein; 290 AA.
 AC AAP83002;
 DT 12-JAN-1991 (first entry)
 DE Sequence of P-2 protein of *Bacillus thuringiensis* var. *kurstaki*.
 KM Insecticide; lepidoptera; diptera; P-2 delta-endotoxin;
 KM parasporal crystal protein.
 OS *Bacillus thuringiensis*.
 XX MO8808034-A.
 XX 20-OCT-1988.
 XX 07-APR-1988; 88MO-US01132.
 XX 16-APR-1987; 87US-0039542.
 PA (ECOG-) ECOGEN INC.
 PI Donovan WP;
 DR WPI; 1988-307569/43.
 DR N-PSDB; AAN80591.
 XX *Bacillus thuringiensis* P-2 toxic gene and expressed protein -
 PT used in insecticidal compns. having activity against
 PT lepidoptera and diptera insects
 PS Claim 10; Fig 2(1) and Fig 2(3); 66pp; English.
 CC A gene for *Bacillus thuringiensis* (B.t.) P-2 toxin having the DNA
 CC sequence specified in Fig 2 (AAN80591), or any portion or deriv. of it,
 CC is claimed. Also claimed is the protein encoded by the gene, having the
 CC corresponding specified AA sequence in AAP83002. In isolating the P-2
 CC gene, the P-2 protein was purified from a donor strain of B.t var.
 CC kurstaki and the partial AA sequence of the P-2 protein was determined.
 CC P-2 gene-specific oligo probe (AAN80590) was synthesized based on the AA
 CC sequence. The P-2 toxin encoded by the cloned gene has insecticidal
 CC activity against lepidoptera and diptera insects.
 CC N.B. The DNA/protein sequence in AAN80591/P83002 is as given in the
 CC specifications and is missing bases 901-1000 and the corresp. AAs.
 XX Sequence 290 AA;
 SQ

Query Match 38.5%; Score 1274.5; DB 9; Length 290;
 Best Local Similarity 46.2%; Pred. No. 11e-94;
 Matches 271; Conservative 13; Mismatches 3; Indels 299; Gaps 1;

QY 1 MNNTLVNNGRTTICDANNVVAHDPSFEHKSIDTIRKEMWKKRTDHSLYAPVGTSSSF 60
 DB 1 MNNTLVNNGRTTICDANNVVAHDPSFEHKSIDTIRKEMWKKRTDHSLYAPVGTSSSF 60

QY 61 LKKVSLIGKRTLSLWGLIFPSGSTNLMODILRETEQFLNCHLNTDLARVNAEGL 120
 DB 61 LKKVSLIGKRTLSLWGLIFPSGSTNLMODILRETEQFLNCHLNTDLARVNAEGL 120
 QY 121 QANIREFNOQVDNPLNPTONPVPLSTSSVNTWQQLFLNRLPQRFVQQLLLPLFAQA 180
 DB 121 QANIREFNOQVDNPLNPTONPVPLSTSSVNTWQQLFLNRLPQRFVQQLLLPLFAQA 180
 QY 181 ANMHLSPIRBYVLANADEWGISAATLFTYONYLKNYTTESNYCINTYQTAFFGNTRLHD 240
 DB 181 ANMHLSPIRBYVLANADEWGISAATLFTYONYLKNYTTESNYCINTYQTAFFGNTRLHD 240
 QY 241 MLEPRTYVPLNVEEYVLSLFTKYSLLVSSGANLYAGSGPQOTQSFISQMPFLYSLF 300
 DB 241 MLEPRTYV----- 248
 QY 301 QVNSNYVLNFGSGARLTQTFPNIGLPGTTTTALLAARVYSGVSSGDIGAVFNQNS 360
 DB 249 ----- 248
 QY 361 CSTFLPPLLPFVRSWLDGSDRGVNTVNTMQTESFESTLGRCAFTARGNSNYPDY 420
 DB 249 ----- 248
 QY 421 FTRISGVPLVARNEDLRRLPHYNEIRNIESPSGTPGLARVMSVNRKNNTIYAVHENG 480
 DB 249 ----- 248
 QY 481 TMHILAPEDYTGFTISPIHATOVNQTPTFISEKFGNQGDSLRFEGSNTTARYTLRGNG 540
 DB 249 ----- 248

RESULT 14
 AAM31199
 ID AAM31199 standard; protein; 706 AA.
 AC AAM31199;
 DT 13-FEB-1998 (first entry)
 DE *Bacillus popilliae* crystal protein.
 KM Crystal protein; beetle; Scarabaeidae; maybug; cockchafer;
 KM agricultural pest; spore; *Bacillus thuringiensis*; cytolysing protein;
 KM fusion protein; transgenic plant.
 OS *Bacillus popilliae*.
 XX
 FH Key location/Qualifiers
 FT Protein 1..706
 FT /label= crystal protein
 PN DEL19642729-A1.
 XX 24-APR-1997.
 PF 17-OCT-1996; 96DE-1042729.
 PR 18-OCT-1995; 95DE-1040223.
 PA (UYHE-) UNITV HEIDELBERG.
 PI Krieger L, Schmetter W, Zhang J;
 DR WPI; 1997-237512/22.
 DR N-PSDB; AAT89348.
 XX

PT DNA encoding *Bacillus popilliae* crystal protein - for production of
PT recombinant protein and transgenic plants resistant to attack by
beetles

PS Claim 8; Pages 8-11; 12pp; German.

CC This sequence represents a novel bacterial crystal protein which can be
CC used to control beetles of the family Scarabaeidae, especially
CC *Melolontha* spp. (e.g. maybugs, cockchafer) which are pests of
CC agriculture and forestry. The protein can inhibit eating, killing both
CC adult beetles and larvae. It can be incorporated into eradication
CC programmes involving *Bacillus popilliae* and *Bacillus thuringiensis*
CC spores, fungal spores or cytotoxic proteins in the form of a fusion
CC protein. The DNA can also be used to produce transgenic plants that are
CC resistant to attack by the beetles.

CC Sequence 706 AA;

Query Match 32.6%; Score 1082; DB 18; Length 706;
Best Local Similarity 38.6%; Pred. No. 1.5e-78;
Matches 265; Conservative 95; Mismatches 233; Indels 94; Gaps 21;

QY 2 NNYLAN-----GRITICDA-----YNYAHDPSPFHSKSLDTIRKEMEKRTD 45
DB 58 NNDNNNDACI CDELGTIDNNITICSTDTFTPIVNRDTP--FKKSTQELTREWTEWRENS 115
QY 46 HSLVYVPIVGTSSFLIKKVSLLGRILSELMLIPFGSGTNLMODILRETOFLNORT 105
DB 116 PSLETPAIVGVVTSFLLOSILKQATSFLKTLTDLIFPNNSLSLIEILRATQGYQENL 175
QY 106 NNDTLARVAELEGLOANIREFNOVDNLFNPNPISSTSSNTMOCFLNRLPOR 165
DB 176 DDTANRVSQELVGLKNNLTTRNDYEDFELNKGISPLAIDISINTMOFLVNRLLPOR 235
QY 166 VGGYQLLLPLFAQANMHLSTIRDVYNADENWISATLRTYQYLNKYTEYSNYCN 225
DB 236 VSGYVLLPLFAQATLHLTFLRDLVILNADENWITFAOLNNTYEFEXYAEYSNVALS 295
QY 226 TYQTAFRGANTR-----LHDLERTYMFNVREYSIWSLFKKYQLSLVSGANIXASG 279
DB 296 TYDGEFR---TRFYPNTLEDMLQKRTMTLMDLVSIMSLAKYMLVSTANLXNIG 352
QY 280 SGPQOTGFTSQDMPFLYSLFQVNSNYLNGFSGARLTQTFENIG-----LPGTTTTH 333
DB 353 DNKNVGAFFISYGFPPFNSYIQTKSNVYLSGVSGIGARFTYTVLGRYLHDLKNITTT- 411
QY 334 ALLARVYSGVSSGSDIGAVFN-----ONFSCSTFLP-PLNLP 371
DB 412 -----YVGTOGGINIGVQLSTTEDELKQQQATRLSDVDFQFTLMCMLEPITAP 463
QY 372 -FVNSMLDSC-SDRGVNTVTNMQTESFESTGL-RQGAFTARGSNYPFDYFIRNISGV 428
DB 464 YFATSLYESRYSISIGGYLKKDFKSE--DSTCGAGNPGAMTS-----YDYTYINISAT 515
QY 429 PLVANNEDLRPLAHYEIRNISPSGTPGGRLAAYVWVSNNKNIIVAHENGMIHAP 488
DB 516 VQINGEMTDTPFLYFENRPISTRGV-----NKVAYVNRKANIAGTNGMTHQAP 570
QY 489 DYTGFTISPIHATQVNNQRTFISEKFGQSDSLRFEOSNTTAYTLRNG-NSNYLYR 547
DB 571 DGTGFTVSPHPSA--NTITSYIKENYNGSDSLHL-KGQGYLHYMLSGGQDRYRLVIR 627
QY 548 VSSLGNTIIRVTINGEVYTAGSVNTTNNQDVNDGAPFLINNGN--VVASDNTNVPLD 605
DB 628 LSGAAN---QIKQSTTISIVAFDSTINNEGITDNGSKFQPAFSTFVPIBOK-----E 679
QY 606 INTFNSGTFELAMINMFVNTNLPPIY 632
DB 680 IVLTFEGVSLDMLNLIPLADDPFLY 706

RESULT 15
AAP81356

ID AAP81356 standard; protein; 99 AA.

AC AAP81356;

DT 12-JAN-1991 (first entry)

DE Sequence of fragment of *Bacillus thuringiensis* P-2 protein.

KW Insecticide; lepidoptera; diptera; P-2 delta-endotoxin;
KW parasporal crystal protein.

OS *Bacillus thuringiensis*.

FN W08808034-A.

PD 20-OCT-1988.

PF 07-APR-1988; 88WC-US01132.

PR 16-APR-1987; 87US-0039542.

PA (ECOG-) ECOGEN INC.

PI Donovan WP;

DR WPI; 1988-307569/43.

PT *Bacillus thuringiensis* P-2 toxin gene and expressed protein -
PT used in insecticidal compns. having activity against
PT lepidoptera and diptera insects

PS Claim 73; Fig 6 and Page 54; 66pp; English.

CC A gene for *Bacillus thuringiensis* (B.t.) P-2 toxin having the DNA
CC sequence specified in Fig 2 (AAN80591), or any portion or deriv. of it,
CC is claimed. Also claimed is the protein encoded by the gene, having the
CC corresponding specified AA sequence in AAN80548. In isolating the P-2
CC gene, the P-2 protein was purified from a donor strain of B.t. var.
CC kurstaki and the partial AA sequence of the P-2 protein was determined.
CC P-2 gene-specific oligo probe (AAN80590) was synthesised based on the AA
CC sequence. The P-2 toxin encoded by the cloned gene has insecticidal
CC activity against lepidoptera and diptera insects. SQ corresponds to
CC residues 162-260 of the P-2 protein.

CC Sequence 99 AA;

Query Match 15.1%; Score 499; DB 9; Length 99;
Best Local Similarity 91.9%; Pred. No. 1.2e-32;
Matches 91; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 162 POPRVOGYQLLLPLFAQANMHLSTIRDVYNADENWISATLRTYQYLNKYTEYSN 221
DB 1 PQRIGQYQLLLPLFAQANMHLSTIRDVYNADENWISATLRTYQYLNKYTEYSN 60

QY 222 YCINTYOTAFRGANTRHDLMEFRFTYMFNVREYSIMS 260
DB 61 YCINTYOTAFRGANTRHDLMEFRFTYMFNVREYSIMS 99

Search completed: August 14, 2003, 18:11:01
Job time : 53 secs

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OM protein - protein search, using sw model

Run on: August 14, 2003, 18:10:07 ; Search time 30 Seconds
(without alignments)
891.349 Million cell updates/sec

Title: US-10-040-906a-2
Perfect score: 3314
Sequence: 1 MNVYNGRTTICDAVNVVA.....GTQPELKNIMPTNLPY 632

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/6C.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/6D.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3043.5	91.8	634	US-09-186-002-12	Sequence 12, Appl
2	3015.5	91.0	635	US-09-041-991A-4	Sequence 4, Appl
3	3015.5	91.0	635	US-09-608-533A-4	Sequence 4, Appl
4	3010.5	90.8	633	US-09-186-002-18	Sequence 18, Appl
5	3005.5	90.7	634	US-09-186-002-2	Sequence 2, Appl
6	2914.5	87.9	633	US-09-041-991A-10	Sequence 10, Appl
7	2914.5	87.9	633	US-09-608-533A-10	Sequence 10, Appl
8	2913.5	87.9	633	US-09-041-991A-8	Sequence 8, Appl
9	2913.5	87.9	633	US-09-608-533A-8	Sequence 8, Appl
10	2610.5	78.8	623	US-09-041-991A-6	Sequence 6, Appl
11	1080	32.6	706	US-09-608-533A-6	Sequence 6, Appl
12	336.5	10.2	644	US-08-793-331-7	Sequence 7, Appl
13	327.5	9.9	648	US-08-286-870A-4	Sequence 4, Appl
14	327.5	9.9	719	US-08-286-870A-8	Sequence 8, Appl
15	327.5	9.9	719	US-08-286-870A-8	Sequence 8, Appl
16	311.5	9.4	1156	US-09-002-285-72	Sequence 72, Appl
17	311.5	9.4	1156	US-09-589-477-72	Sequence 72, Appl
18	307	9.3	1157	US-08-532-547-5	Sequence 5, Appl
19	307	9.3	1157	US-08-379-656B-5	Sequence 5, Appl
20	307	9.3	1157	US-08-455-838-5	Sequence 5, Appl
21	307	9.3	1157	US-09-019-809-7	Sequence 9, Appl
22	307	9.3	1157	US-09-019-809-5	Sequence 5, Appl
23	306	9.2	1138	US-09-471-177-5	Sequence 5, Appl
24	306	9.2	1138	US-07-973-320-2	Sequence 2, Appl
25	305.5	9.2	1138	US-07-973-320-4	Sequence 4, Appl
26	305.5	9.2	1186	US-09-178-252-23	Sequence 23, Appl
27	305.5	9.2	1227	US-08-448-170-8	Sequence 8, Appl

28	305.5	9.2	1227	US-08-961-803-9	Sequence 9, Appl
29	304.5	9.2	625	US-08-532-547-7	Sequence 7, Appl
30	304.5	9.2	625	US-08-532-547-9	Sequence 9, Appl
31	304.5	9.2	625	US-09-019-809-7	Sequence 9, Appl
32	304.5	9.2	625	US-09-019-809-9	Sequence 9, Appl
33	304.5	9.2	625	US-09-019-809-9	Sequence 9, Appl
34	304.5	9.2	625	US-09-471-177-7	Sequence 7, Appl
35	294.5	8.9	1176	US-08-434-823-2	Sequence 2, Appl
36	294.5	8.9	1176	US-08-457-366-2	Sequence 2, Appl
37	293.5	8.9	1229	US-08-100-709-4	Sequence 4, Appl
38	293.5	8.9	1229	US-08-176-865-4	Sequence 4, Appl
39	293.5	8.9	1229	US-08-474-038-4	Sequence 4, Appl
40	293.5	8.9	1229	US-08-779-046-4	Sequence 4, Appl
41	293.5	8.9	1229	US-08-881-340-4	Sequence 4, Appl
42	292	8.8	488	US-08-448-170-10	Sequence 10, Appl
43	292	8.8	488	US-08-448-170-10	Sequence 10, Appl
44	291.5	8.8	1179	US-08-961-803-10	Sequence 10, Appl
45	288.5	8.7	1176	US-07-828-768A-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-186-002-12
; Sequence 12, Application US/09186002B
; Patent No. 6489542
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; TITLE OF INVENTION: Improved Method for Transforming Plants to Express
; FILE REFERENCE: 38-21(13547) US Pat No. 6489542 09/186,002
; CURRENT FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO: 12
; LENGTH: 634
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-09-186-002-12

Query Match	91.8%	Score 3043.5	DB 4	Length 634
Best Local Similarity	90.7%	Pred. No. 1.4e-262		
Matches 573	Conservative 34	Mismatches 24	Indels 1	Gaps 1
QY	2	NNVYNGRTTICDAVNVVAHDPFSEKESLDTIRKEMEMKRTDHSIYVPIGVYSSPL	61	
DB	3	NNVYNGRTTICDAVNVVAHDPFSEKESLDTIRKEMEMKRTDHSIYVPIGVYSSPL	62	
QY	62	LKKGSLIGRIISLWGLIPFGSTLMODILRETEQFLNORLNTDTTARVNALEGLQ	121	
DB	63	LKKGSLIGRIISLWGLIPFGSTLMODILRETEQFLNORLNTDTTARVNALEGLQ	122	
QY	122	ANIREFOQVDFNLFNPQVPLSITSSVNTMOOLFNLRLPQFVQGYQLLPIFAQA	181	
DB	123	ANIREFOQVDFNLFNPQVPLSITSSVNTMOOLFNLRLPQFVQGYQLLPIFAQA	182	
QY	182	NHLSFIRVDVNAADKWSIAATRTQYLNKTYTESNCTINTYGAARGLRLHDM	241	
DB	183	NHLSFIRVDVNAADKWSIAATRTQYLNKTYTESNCTINTYGAARGLRLHDM	242	
QY	242	LEFRTYFLNVEFYVSIWLFKQSLVSGANLYASGSGPQOTSGTQDPFLYSDFQ	301	
DB	243	LEFRTYFLNVEFYVSIWLFKQSLVSGANLYASGSGPQOTSGTQDPFLYSDFQ	302	
QY	302	VNSVYVANGSGARLTQTEPNIGLPGTTTHALLAARVYSGVSSDGLGV-FNQFS	360	
DB	303	VNSVYVANGSGARLTQTEPNIGLPGTTTHALLAARVYSGVSSDGLGV-FNQFS	362	
QY	361	CSTLPPLLPVRSWMDSGSDRGVYVTVNQTSEFSTLGLRCGAPFARNGSNVYFDDY	420	

Db 363 CSTVLPPLSTPFRWSMDSGTDRGVATSTMTQTESFQITLSIRCGAFSAGNSNTPPY 422

Qy 421 FTRISGVPLVVRNEDLRPLHYNEIRNIESPSGTGGRLAYVSVHNRKNYIAVHENG 480

Db 423 FTRISGVPLVVRNEDLRPLHYNQIRNIESPSGTGGARAYVSVHNRKNYIAVHENG 482

Qy 481 TMTLAPEDYTGFTTSPHATQVNNQTRFISEKFGNQGOSLPEQOSNTTARVTLRGNG 540

Db 483 TMTLAPEDYTGFTTSPHATQVNNQTRFISEKFGNQGOSLPEQOSNTTARVTLRGNG 542

Qy 541 SYNTLAVSSIGNSTIRVTINGRVYTVASNVNTTNNDSVNDNGARFLDINMGAVASDNT 600

Db 543 SYNTLAVSSIGNSTIRVTINGRVYTVASNVNTTNNDSVNDNGARFLDINMGAVASDNT 602

Qy 601 NVPLDINVTNSGTQFELNMIMFVPTNLPPLY 632

Db 603 NVPLDINVTNSGTQFELNMIMFVPTNLPPLY 634

RESULT 2

US-09-041-991A-4

/ Sequence 4, Application US/09041991A

/ Patent No. 6107278

/ GENERAL INFORMATION:

/ APPLICANT: Schepf, H. Ernest

/ APPLICANT: Narva, Kenneth E.

/ APPLICANT: Muller-Cohn, Judy

/ TITLE OF INVENTION: Toxins Active Against Pests

/ NUMBER OF SEQUENCES: 10

/ CORRESPONDENCE ADDRESS:

/ ADDRESS: Saliwanichik, Lloyd & Saliwanichik

/ STREET: 2421 N.W. 41st Street, Suite A-1

/ CITY: Gainesville

/ STATE: Florida

/ COUNTRY: USA

/ ZIP: 32606

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patent in

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/09/041,991A

/ FILING DATE: 13-MAR-1998

/ CLASSIFICATION: 514

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Sanders, Jay M.

/ REGISTRATION NUMBER: 39,355

/ REFERENCE/DOCKET NUMBER: MA-709

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (352) 372-5800

/ TELEFAX: (352) 372-5800

/ INFORMATION FOR SEQ ID NO: 4:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 635 amino acids

/ TYPE: amino acid

/ STRANDEDNESS: single

/ TOPOLOGY: linear

/ MOLECULE TYPE: peptide

/ US-09-041-991A-4

Query Match 91.0%; Score 3015.5; DB 3; Length 635;

Best Local Similarity 90.2%; Pred. No. 4.3e-260;

Matches 573; Conservative 30; Mismatches 29; Indels 3; Gaps 2;

Qy 1 MNVUNNGRTTCDAVYVVAHDPFSEHKSJDTIRKEMEMKRTDHSIYVAPIVGVSSF 60

Db 1 MNVUNNGRTTCDAVYVVAHDPFSEHKSJDTIRKEMEMKRTDHSIYVAPIVGVSSF 60

Qy 61 LKKVGSILIGRIISELMGLIFPSSGNTNMODIIRFEOVLNRQNLNTTTLARVNAELFGL 120

Db 61 LKKVGSILIGRIISELMGLIFPSSGNTNMODIIRFEOVLNRQNLNTTTLARVNAELFGL 120

Qy 121 QANIREFNOQVDFNLPNTONPVPLSTITTSVNTQOQLFNLRPFRVQYQILLPLFPAQ 180

Db 121 QANIREFNOQVDFNLPNTONPVPLSTITTSVNTQOQLFNLRPFRVQYQILLPLFPAQ 180

Qy 181 ANKHLSPTRDVLNADBNKISAACTRTQVLYLKNYTTESVNCINTYQTFRGANTRLHD 240

Db 181 ANKHLSPTRDVLNADBNKISAACTRTQVLYLKNYTTESVNCINTYQTFRGANTRLHD 240

Qy 241 MLEFRTYFLNVEFEYSIMSLFKYQSLVSSGANLYVSGSGPQOTGTSQDMPPLYSLF 300

Db 241 MLEFRTYFLNVEFEYSIMSLFKYQSLVSSGANLYVSGSGPQOTGTSQDMPPLYSLF 300

Qy 301 QVNSVYVNGSGSGLRQTFPPNIGLPGTTTALLAARVNSGVSSGDIQAV-ENQF 359

Db 301 QVNSVYVNGSGSGLRQTFPPNIGLPGTTTALLAARVNSGVSSGDIQAV-ENQF 359

Qy 360 SCSTFLPPLLPFRWSMDSGSDRGVNTVNNQTESFESTYGLRGA--FYARGNSYF 417

Db 361 NCSTVLPPLSTPFRWSMDSGTDRGVATSTMTQTESFQITLSIRCGAFPSAGNSNTP 420

Qy 418 PDYFTRISGVPLVVRNEDLRPLHYNEIRNIESPSGTGGRLAYVSVHNRKNYIAVH 477

Db 421 PDYFTRISGVPLVVRNEDLRPLHYNQIRNIESPSGTGGRLAYVSVHNRKNYIAVH 480

Qy 478 ENGMTHLAPEDYTGFTTSPHATQVNNQTRFISEKFGNQGOSLPEQOSNTTARVTLRG 537

Db 481 ENGMTHLAPEDYTGFTTSPHATQVNNQTRFISEKFGNQGOSLPEQOSNTTARVTLRG 540

Qy 538 NGNSVLYLRVSSIGNSTIRVTINGRVYTVASNVNTTNNDSVNDNGARFLDINMGAVAS 597

Db 541 NGNSVLYLRVSSIGNSTIRVTINGRVYTVASNVNTTNNDSVNDNGARFLDINMGAVAS 600

Qy 598 DNTNVPDLINVTNSGTQFELNMIMFVPTNLPPLY 632

Db 601 DNTNVPDLINVTNSGTQFELNMIMFVPTNLPPLY 635

RESULT 3

US-09-608-533A-4

/ Sequence 4, Application US/09608533A

/ Patent No. 6534644

/ GENERAL INFORMATION:

/ APPLICANT: Schepf, H. Ernest

/ APPLICANT: Narva, Kenneth E.

/ APPLICANT: Muller-Cohn, Judy

/ TITLE OF INVENTION: Toxins Active Against Pests

/ NUMBER OF SEQUENCES: 10

/ CORRESPONDENCE ADDRESS:

/ ADDRESS: Saliwanichik, Lloyd & Saliwanichik

/ STREET: 2421 N.W. 41st Street, Suite A-1

/ CITY: Gainesville

/ STATE: Florida

/ COUNTRY: USA

/ ZIP: 32606

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patent in

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/09/608,533A

/ FILING DATE: 30-Jun-2000

/ CLASSIFICATION: <Unknown>

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 09/041,991

/ FILING DATE: 13-MAR-1998

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Sanders, Jay M.

/ REGISTRATION NUMBER: 39,355

/ REFERENCE/DOCKET NUMBER: MA-709D1

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (352) 372-5800

/ TELEFAX: (352) 372-5800

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 635 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-608-533A-4

Query Match 91.0%; Score 3015.5; DB 4; Length 635;
Best Local Similarity 90.2%; Pred. No. 4,3e-260;

Matches 573; Conservative 30; Mismatches 29; Indels 3; Gaps 2;

```
QY 1 MNNVINGRTTICDANNVVAADPFSEHKSJDTIRKEMEMKATDHSLYVAPVIGTVSSP 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MNNVINGRTTICDANNVVAADPFSEHKSJDTIRKEMEMKATDHSLYVAPVIGTVSSP 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 LKKVSGSLIGKRILSELWGLIFPSGSTNIMODILRETEQFLNORLNTDTLARVAELEG 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 LKKVSGSLIGKRILSELWGLIFPSGSTNIMODILRETEQFLNORLNTDTLARVAELEG 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 QANIRENOQVDNPLNPNPVPPLSTSSVNTMOQLFLNRLPQFVQYQLLLPLPAQA 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 QANIRENOQVDNPLNPNPVPPLSTSSVNTMOQLFLNRLPQFVQYQLLLPLPAQA 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 ANHLSFTRDVVLANDEWGISATLRTYONYLKNYTEREYNYCINTYOTAFRGALNRLHD 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 ANHLSFTRDVVLANDEWGISATLRTYONYLKNYTEREYNYCINTYOTAFRGALNRLHD 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 MLEPRTYMFANVEFYVSIWLSFKYOSLLVSGANLYASGSGPOQTOSFTSQDMPFLYSLE 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 MLEPRTYMFANVEFYVSIWLSFKYOSLLVSGANLYASGSGPOQTOSFTSQDMPFLYSLE 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 301 QVNSNVTNLNGSGARLVTQEPNIGLPGTTTHALLAARVNSGVSAGDIGA-VEFNONE 359
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Db 301 QVNSNVTNLNGSGARLVTQEPNIGLPGTTTHALLAARVNSGVSAGDIGA-VEFNONE 359
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 360 SCSTFLPPLLPFRVSWLSDSGDRGVNTVNTMOTESPESTGLRGA-ETAKGNENYF 417
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Db 360 SCSTFLPPLLPFRVSWLSDSGDRGVNTVNTMOTESPESTGLRGA-ETAKGNENYF 417
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 418 PDYFRINISGVPLVVRNEDLRPLAHNEIRNIESPSGTPGGLRAYVWSVHNRKNNIYAAH 477
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 418 PDYFRINISGVPLVVRNEDLRPLAHNEIRNIESPSGTPGGLRAYVWSVHNRKNNIYAAH 477
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 478 ENGTMHLAPEDYGTFTSPHATOVNNOQRTFISEKFGQGSILRFEOSNTTARVTLRG 537
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 478 ENGTMHLAPEDYGTFTSPHATOVNNOQRTFISEKFGQGSILRFEOSNTTARVTLRG 537
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 538 NGNSVYLKRVSSLSGNSITRTVINGRVYTAASVNTTNDGVNDGAFDLINMGVVAS 597
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 538 NGNSVYLKRVSSLSGNSITRTVINGRVYTAASVNTTNDGVNDGAFDLINMGVVAS 597
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 541 NGNSVYLKRVSSLSGNSITRTVINGRVYTAASVNTTNDGVNDGAFDLINMGVVAS 600
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 541 NGNSVYLKRVSSLSGNSITRTVINGRVYTAASVNTTNDGVNDGAFDLINMGVVAS 600
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 598 DNTNVPDLINVTNSGTQFELMINIMVPTNLPY 632
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 598 DNTNVPDLINVTNSGTQFELMINIMVPTNLPY 632
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 601 DNTNVPDLINVTNSGTQFELMINIMVPTNLPY 635
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 601 DNTNVPDLINVTNSGTQFELMINIMVPTNLPY 635
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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RESULT 4
US-09-186-002-18
; Sequence 18, Application US/09186002B
; Patent No. 6489542
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Method for Transforming Plants to Express
; FILE REFERENCE: 38-21(13547) US Pat No. 6489542 09/186,002
; CURRENT APPLICATION NUMBER: US/09/186,002B
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0; SEQ ID NO 18
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; US-09-186-002-18Query Match 90.8%; Score 3010.5; DB 4; Length 633;
Best Local Similarity 89.7%; Pred. No. 1,2e-259;
Matches 568; Conservative 39; Mismatches 25; Indels 1; Gaps 1;

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QY 1 MNNVINGRTTICDANNVVAADPFSEHKSJDTIRKEMEMKATDHSLYVAPVIGTVSSP 60
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Db 1 MNNVINGRTTICDANNVVAADPFSEHKSJDTIRKEMEMKATDHSLYVAPVIGTVSSP 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 LKKVSGSLIGKRILSELWGLIFPSGSTNIMODILRETEQFLNORLNTDTLARVAELEG 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 LKKVSGSLIGKRILSELWGLIFPSGSTNIMODILRETEQFLNORLNTDTLARVAELEG 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 QANIRENOQVDNPLNPNPVPPLSTSSVNTMOQLFLNRLPQFVQYQLLLPLPAQA 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 QANIRENOQVDNPLNPNPVPPLSTSSVNTMOQLFLNRLPQFVQYQLLLPLPAQA 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 ANHLSFTRDVVLANDEWGISATLRTYONYLKNYTEREYNYCINTYOTAFRGALNRLHD 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 ANHLSFTRDVVLANDEWGISATLRTYONYLKNYTEREYNYCINTYOTAFRGALNRLHD 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 MLEPRTYMFANVEFYVSIWLSFKYOSLLVSGANLYASGSGPOQTOSFTSQDMPFLYSLE 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 MLEPRTYMFANVEFYVSIWLSFKYOSLLVSGANLYASGSGPOQTOSFTSQDMPFLYSLE 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 301 QVNSNVTNLNGSGARLVTQEPNIGLPGTTTHALLAARVNSGVSAGDIGA-VEFNONE 359
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 QVNSNVTNLNGSGARLVTQEPNIGLPGTTTHALLAARVNSGVSAGDIGA-VEFNONE 359
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 360 SCSTFLPPLLPFRVSWLSDSGDRGVNTVNTMOTESPESTGLRGA-ETAKGNENYF 419
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 360 SCSTFLPPLLPFRVSWLSDSGDRGVNTVNTMOTESPESTGLRGA-ETAKGNENYF 419
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 418 PDYFRINISGVPLVVRNEDLRPLAHNEIRNIESPSGTPGGLRAYVWSVHNRKNNIYAAH 479
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 418 PDYFRINISGVPLVVRNEDLRPLAHNEIRNIESPSGTPGGLRAYVWSVHNRKNNIYAAH 479
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 478 ENGTMHLAPEDYGTFTSPHATOVNNOQRTFISEKFGQGSILRFEOSNTTARVTLRG 539
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 478 ENGTMHLAPEDYGTFTSPHATOVNNOQRTFISEKFGQGSILRFEOSNTTARVTLRG 539
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 538 NGNSVYLKRVSSLSGNSITRTVINGRVYTAASVNTTNDGVNDGAFDLINMGVVAS 599
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 538 NGNSVYLKRVSSLSGNSITRTVINGRVYTAASVNTTNDGVNDGAFDLINMGVVAS 599
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 541 NGNSVYLKRVSSLSGNSITRTVINGRVYTAASVNTTNDGVNDGAFDLINMGVVAS 600
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 541 NGNSVYLKRVSSLSGNSITRTVINGRVYTAASVNTTNDGVNDGAFDLINMGVVAS 600
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QY 600 TNPVLDINVTNSGTQFELMINIMVPTNLPY 632
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 600 TNPVLDINVTNSGTQFELMINIMVPTNLPY 632
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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RESULT 5
US-09-186-002-2
; Sequence 2, Application US/09186002B
; Patent No. 6489542
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Method for Transforming Plants to Express
; FILE REFERENCE: 38-21(13547) US Pat No. 6489542 09/186,002
; CURRENT APPLICATION NUMBER: US/09/186,002B
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 634
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis

Fri Aug 15 11:51:34 2003

us-10-040-906a-2.rat

Page 4

US-09-186-002-2

Query Match 90.7%; Score 3005.5; DB 4; Length 634;
Best Local Similarity 89.7%; Pred. No. 3.3e-259;
Matches 567; Conservative 39; Mismatches 25; Indels 1; Gaps 1;

QY 2 NNNVNNNGRTTICAYNVVVAHDPFSEFHKSLDITRKEMEMKRDHSLYVAPVIGVTSFL 61
DB 3 NSVNSGRITTCAYNVVVAHDPFSEFHKSLDITRKEMEMKRDHSLYVAPVIGVTSFL 62
QY 62 LKTVSLIGKRLISELMGLIFPSSGNTLMODILRETEFLNORLNTDTLAVNAELLEG 121
DB 63 LKTVSLIGKRLISELMGLIFPSSGNTLMODILRETEFLNORLNTDTLAVNAELLEG 122
QY 122 ANIEFNOQVNDNFNTONPVPLSTTSVNTMOQLFRLRPOFVOCYQLLPLFAQA 181
DB 123 ANIEFNOQVNDNFNTONPVPLSTTSVNTMOQLFRLRPOFVOCYQLLPLFAQA 182
QY 182 NMHLSPTRDVLNADDEWGISATLRTYQNYLKNYTESNYCINTYQTAFLGRLRLHD 241
DB 183 NMHLSPTRDVLNADDEWGISATLRTYQNYLKNYTESNYCINTYQTAFLGRLRLHD 242
QY 242 LEFRTYMLNVEFYVNSLFFKQSLVSSGANLYASGSGPOQTSQDMPFLYSLFQ 301
DB 243 LEFRTYMLNVEFYVNSLFFKQSLVSSGANLYASGSGPOQTSQDMPFLYSLFQ 302
QY 302 VNSNVYLVNGSGARLTQTFPNIGLPGTTTHALLAARVNTSGVSSGDI- GAVENQNF 360
DB 303 VNSNVYLVNGSGARLTQTFPNIGLPGTTTHALLAARVNTSGVSSGDI- GAVENQNF 362
QY 361 CSTFLPPLTTPFVRSWLDGSGRGVNTVMQTESFESTGLRCGAFARAGNSNFPDY 420
DB 363 CSTFLPPLTTPFVRSWLDGSGRGVNTVMQTESFESTGLRCGAFARAGNSNFPDY 422
QY 421 FTRNIGVPLVVRNEDLRPLHYNEIRNIESPGTCGRLAMVSYNEKNNIYVHNG 480
DB 423 FTRNIGVPLVVRNEDLRPLHYNEIRNIESPGTCGRLAMVSYNEKNNIYVHNG 482
QY 481 TWIHLAPEDYGTISPIHATOVNQTTFISEFGNQGDSLRFGSNTTARVTLRNGN 540
DB 483 TWIHLAPEDYGTISPIHATOVNQTTFISEFGNQGDSLRFGSNTTARVTLRNGN 542
QY 541 SYNLVLRVSSLSNGSTIRVYTAASVNTTNDGVNDGARFSDINMGVVASDNT 600
DB 543 SYNLVLRVSSLSNGSTIRVYTAASVNTTNDGVNDGARFSDINMGVVASDNT 602
QY 601 NVPLDINTVNSGTOFELNMIMFVPTNLPLY 632
DB 603 NVPLDINTVNSGTOFELNMIMFVPTNLPLY 634

RESULT 6
US-09-041-991A-10
Sequence 10, Application US/09041991A
Patent No. 6107278
GENERAL INFORMATION:
APPLICANT: Schuepf, H. Ernest
APPLICANT: Narva, Kenneth E.
APPLICANT: Miller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,991A
FILING DATE: 13-MAR-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-709
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 633 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-041-991A-10

Query Match 87.9%; Score 2914.5; DB 3; Length 633;
Best Local Similarity 87.0%; Pred. No. 4.3e-251;
Matches 551; Conservative 44; Mismatches 37; Indels 1; Gaps 1;

QY 1 MNNVNNNGRTTICAYNVVVAHDPFSEFHKSLDITRKEMEMKRDHSLYVAPVIGVTSFL 60
DB 1 MNNVNNNGRTTICAYNVVVAHDPFSEFHKSLDITRKEMEMKRDHSLYVAPVIGVTSFL 60
QY 61 LKTVSLIGKRLISELMGLIFPSSGNTLMODILRETEFLNORLNTDTLAVNAELLEG 120
DB 61 LKTVSLIGKRLISELMGLIFPSSGNTLMODILRETEFLNORLNTDTLAVNAELLEG 120
QY 121 ANIEFNOQVNDNFNTONPVPLSTTSVNTMOQLFRLRPOFVOCYQLLPLFAQA 180
DB 121 ANIEFNOQVNDNFNTONPVPLSTTSVNTMOQLFRLRPOFVOCYQLLPLFAQA 180
QY 181 NMHLSPTRDVLNADDEWGISATLRTYQNYLKNYTESNYCINTYQTAFLGRLRLHD 240
DB 181 NMHLSPTRDVLNADDEWGISATLRTYQNYLKNYTESNYCINTYQTAFLGRLRLHD 240
QY 241 MLEFRTYMLNVEFYVNSLFFKQSLVSSGANLYASGSGPOQTSQDMPFLYSLF 300
DB 241 MLEFRTYMLNVEFYVNSLFFKQSLVSSGANLYASGSGPOQTSQDMPFLYSLF 300
QY 301 QVNSNVYLVNGSGARLTQTFPNIGLPGTTTHALLAARVNTSGVSSGDI- GAVENQNF 359
DB 301 QVNSNVYLVNGSGARLTQTFPNIGLPGTTTHALLAARVNTSGVSSGDI- GAVENQNF 360
QY 360 SCSTFLPPLTTPFVRSWLDGSGRGVNTVMQTESFESTGLRCGAFARAGNSNFPDY 419
DB 361 SCSTFLPPLTTPFVRSWLDGSGRGVNTVMQTESFESTGLRCGAFARAGNSNFPDY 420
QY 420 YFIRNIGVPLVVRNEDLRPLHYNEIRNIESPGTCGRLAMVSYNEKNNIYVHNG 479
DB 421 YFIRNIGVPLVVRNEDLRPLHYNEIRNIESPGTCGRLAMVSYNEKNNIYVHNG 480
QY 480 GTMHLAPEDYGTISPIHATOVNQTTFISEFGNQGDSLRFGSNTTARVTLRNG 539
DB 481 GTMHLAPEDYGTISPIHATOVNQTTFISEFGNQGDSLRFGSNTTARVTLRNG 540
QY 540 NSYLVLRVSSLSNGSTIRVYTAASVNTTNDGVNDGARFSDINMGVVASDNT 599
DB 541 NSYLVLRVSSLSNGSTIRVYTAASVNTTNDGVNDGARFSDINMGVVASDNT 600
QY 600 NVPLDINTVNSGTOFELNMIMFVPTNLPLY 632
DB 601 NVPLDINTVNSGTOFELNMIMFVPTNLPLY 633

RESULT 7
US-09-608-533A-10
Sequence 10, Application US/09608533A
Patent No. 6534644

GENERAL INFORMATION:

APPLICANT: Schnepf, H. Ernest

Narva, Kenneth E.

Muller-Cohn, Judy

TITLE OF INVENTION: Toxins Active Against Peets

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESS: Saliwanchik, Lloyd & Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: Florida

COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/608,533A

FILING DATE: 30-Jun-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/041,991

FILING DATE: 13-MARCH-1998

ATTORNEY/AGENT INFORMATION:

NAME: Sanders, Jay M.

REGISTRATION NUMBER: 39,355

REFERENCE/DOCKET NUMBER: MA-709D1

TELEPHONE: (352) 375-8100

TELEFAX: (352) 372-5800

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 633 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Query Match 87.9%; Score 2914.5; DB 4; Length 633;

-Best Local Similarity 87.0%; Pred. No. 4.3e-251;

Matches 551; Conservative 44; Mismatches 37; Indels 1; Gaps 1;

QY 1 MNNVLANGRITTCDAVNVVHADPFSFEHKSIDTIRKEMWEMKRTDHSIYVAVIVGVSSSF 60

DB 1 MNNVLANGRITTCDAVNVVHADPFSFEHKSIDTIRKEMWEMKRTDHSIYVAVIVGVSSSF 60

QY 61 LKKVGSILGKRIILSELNGLIFPSGSTNLMEDIETREKFNQKNTDITLSRVNAELTGL 120

DB 61 LKKVGSILGKRIILSELNGLIFPSGSTNLMEDIETREKFNQKNTDITLSRVNAELTGL 120

QY 121 QANIREFNOQVDFLNPONPVPLSTSSVNTMOQLFLNRLPQFRVQGYQLLLPLFAQA 180

DB 121 QANIREFNOQVDFLNPONPVPLSTSSVNTMOQLFLNRLPQFRVQGYQLLLPLFAQA 180

QY 181 ANHLSFIRDVVLNADWEGISAATLRTYONVKNITTEYSNVCINTYQAFRGANTLPHD 240

DB 181 ANHLSFIRDVVLNADWEGISAATLRTYONVKNITTEYSNVCINTYQAFRGANTLPHD 240

QY 241 MLERTYMFANFEVYSIWSLFFKQSLVSSGANIYASGGPQOTQSFISQDMPLXSLF 300

DB 241 MLERTYMFANFEVYSIWSLFFKQSLVSSGANIYASGGPQOTQSFISQDMPLXSLF 300

QY 301 QVNSNYVLNGFSGALITQTPENIGLPFTTTTHALLAARVYSGVSSGDI-GAVFNQNF 359

DB 301 QVNSNYVLNGFSGALITQTPENIGLPFTTTTHALLAARVYSGVSSGDI-GAVFNQNF 359

QY 360 SCSTFLPILLTFPVYSWISDSDRGVNTVMWQESPESTLGRGAFARAGSNATFPD 419

DB 360 SCSTFLPILLTFPVYSWISDSDRGVNTVMWQESPESTLGRGAFARAGSNATFPD 419

QY 420 NCATISPLSTSFVMSWIDSGDRQGVTTVMQTESPETTSILRCGAFTRPGNSVYFG 420

DB 420 NCATISPLSTSFVMSWIDSGDRQGVTTVMQTESPETTSILRCGAFTRPGNSVYFG 420

QY 420 YFIRNISGVLVNRNEDLRPLHANEIRISPSGTRGGLAAMVSNRKNNTYAVHEN 479

DB 421 YFIRNISGVLVNRNEDLRPLHANEIRISPSGTRGGLAAMVSNRKNNTYAVHEN 480

QY 480 GIMIHAPEDYTGFTIPSHATOVNNQRTFISKFNQSDSLRFGSNTTARATTLKNG 539

DB 481 GIMIHAPEDYTGFTIPSHATOVNNQRTFISKFNQSDSLRFGSNTTARATTLKNG 540

QY 540 NSYNVLIARVSSIGNSTIRVTINRGVYASVNTTNDGVNDGAFSDINIGVAVSSN 599

DB 541 NSYNVLIARVSSIGNSTIRVTINRGVYASVNTTNDGVNDGAFSDINIGVAVSSN 600

QY 600 TNVPDINVTNSGTQFELNINFEVPTNLPPIY 632

DB 601 SDVFLDINVTNSGTQFELNINFEVPTNLPPIY 633

RESULT 8

US-09-041-991A-8

Sequence 8, Application US/09041991A

Patent No. 6107278

GENERAL INFORMATION:

APPLICANT: Schnepf, H. Ernest

Narva, Kenneth E.

Muller-Cohn, Judy

TITLE OF INVENTION: Toxins Active Against Peets

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESS: Saliwanchik, Lloyd & Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: Florida

COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/041,991A

FILING DATE: 13-MAR-1998

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Sanders, Jay M.

REGISTRATION NUMBER: 39,355

REFERENCE/DOCKET NUMBER: MA-709

TELECOMMUNICATION INFORMATION:

TELEPHONE: (352) 375-8100

TELEFAX: (352) 372-5800

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 633 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

Query Match 87.9%; Score 2913.5; DB 3; Length 633;

-Best Local Similarity 87.2%; Pred. No. 5.3e-251;

Matches 552; Conservative 42; Mismatches 38; Indels 1; Gaps 1;

QY 1 MNNVLANGRITTCDAVNVVHADPFSFEHKSIDTIRKEMWEMKRTDHSIYVAVIVGVSSSF 60

DB 1 MNNVLANGRITTCDAVNVVHADPFSFEHKSIDTIRKEMWEMKRTDHSIYVAVIVGVSSSF 60

QY 61 LKKVGSILGKRIILSELNGLIFPSGSTNLMEDIETREKFNQKNTDITLSRVNAELTGL 120

DB 61 LKKVGSILGKRIILSELNGLIFPSGSTNLMEDIETREKFNQKNTDITLSRVNAELTGL 120

QY 121 QANIREFNOQVDFLNPONPVPLSTSSVNTMOQLFLNRLPQFRVQGYQLLLPLFAQA 180

DB 121 QANIREFNOQVDFLNPONPVPLSTSSVNTMOQLFLNRLPQFRVQGYQLLLPLFAQA 180

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Db 121 QANVEFRQVDNFMENKNAVPLSTISVYTMQQLFMRISQOMOGYQLLLPLFQA 180
Qy 181 ANMLSFIRDVILNADMGISAAITFTYQNYLKNYTERYSNCINTYQTAFCGLTRLD 240
Db 181 ANMLSFIRDVILNADMGISAAITFTYQNYLKNYTERYSNCINTYQTAFCGLTRLD 240
Db 181 ANMLSFIRDVILNADMGISAAITFTYQNYLKNYTERYSNCINTYQTAFCGLTRLD 240
Qy 241 MEFRYVFLNVEEYISLFFKQSLVSGANLYASGSGPOOTOSFTSQDWPELYSLF 300
Db 241 MEFRYVFLNVEEYISLFFKQSLVSGANLYASGSGPOOTOSFTSQDWPELYSLF 300
Qy 301 QVNSNYVINGSGAKLTOTFPNIGLPGTTTHALLAAVYNSGGVSGDI-GAVNQNPF 359
Db 301 QVNSNYVINGSGAKLTOTFPNIGLPGTTTHALLAAVYNSGGVSGDI-GAVNQNPF 359
Qy 301 QVNSNYVINGSGAKLTOTFPNIGLPGTTTHALLAAVYNSGGVSGDI-GAVNQNPF 360
Db 301 QVNSNYVINGSGAKLTOTFPNIGLPGTTTHALLAAVYNSGGVSGDI-GAVNQNPF 360
Qy 360 SCSTFPLPLTPFVRSWLDGSDRGVAVTNMQTESFESTLGLRCGAFARAGSNVFPD 419
Db 361 NCNTISPLSTSPFVRIWLDGSDRGVAVTNMQTESFESTLGLRCGAFARAGSNVYPG 420
Qy 420 YFIRNIGSVPLVYRNEDLRPLHYNEIRNIESPSGTGGARAYVSVHNNKNNIYAHEN 479
Db 421 YFIRNIGSVPLVYRNEDLRPLHYNEIRNIESPSGTGGARAYVSVHNNKNNIYAHEN 480
Qy 480 GTMHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGQSDLRPEOSNTTAYTLRGNG 539
Db 481 GTMHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGQSDLRPEOSNTTAYTLRGNG 540
Qy 540 NSYNLYRVSSLGNSITRTINGRYTASNTTTNDGVNDGNARFLDINMGNYVASDN 599
Db 541 NSYNLYRVSSLGNSITRTINGRYTASNTTTNDGVNDGNARFLDINMGNYVASDN 600
Qy 600 TNPPLDINTVNSGTQFPELMNIMFVPTNLPY 632
Db 601 SDVPLDINTVNSGTQFPELMNIMFVPTNLPY 633

```

RESULT 9
US-09-608-533a-8
Sequence 8, Application US/09608533A
Patent No. 6534644
GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
Narva, Kenneth E.
Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/608,533A
FILING DATE: 30-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/041,991
FILING DATE: 13-MARCH-1998
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39 355
REFERENCE/DOCKET NUMBER: MA-709D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 8:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 633 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-608-533a-8
Query Match 87.9%; Score 2913.5; DB 4; Length 633;
Best Local Similarity 87.2%; Pred. No. 5,3e-251;
Matches 552; Conservative 42; Mismatches 38; Indels 1; Gaps 1;
Qy 1 MANNVANGRTTCDAYNVVADPFSEHKSIDTTRKMMEMKTHDSLYVPIGTSSP 60
Db 1 MANNVANGRTTCDAYNVVADPFSEHKSIDTTRKMMEMKTHDSLYVPIGTSSP 60
Qy 61 LKKVSLIGKILSELWGLIFPSGSTNLMODILRETEOFNORLNTDTLARVNALEGL 120
Db 61 LKKVSLIGKILSELWGLIFPSGSTNLMODILRETEOFNORLNTDTLARVNALEGL 120
Qy 121 QANTRNQVDNFMENKNAVPLSTISVYTMQQLFMRISQOMOGYQLLLPLFQA 180
Db 121 QANTRNQVDNFMENKNAVPLSTISVYTMQQLFMRISQOMOGYQLLLPLFQA 180
Qy 181 ANMLSFIRDVILNADMGISAAITFTYQNYLKNYTERYSNCINTYQTAFCGLTRLD 240
Db 181 ANMLSFIRDVILNADMGISAAITFTYQNYLKNYTERYSNCINTYQTAFCGLTRLD 240
Qy 241 MEFRYVFLNVEEYISLFFKQSLVSGANLYASGSGPOOTOSFTSQDWPELYSLF 300
Db 241 MEFRYVFLNVEEYISLFFKQSLVSGANLYASGSGPOOTOSFTSQDWPELYSLF 300
Qy 301 QVNSNYVINGSGAKLTOTFPNIGLPGTTTHALLAAVYNSGGVSGDI-GAVNQNPF 359
Db 301 QVNSNYVINGSGAKLTOTFPNIGLPGTTTHALLAAVYNSGGVSGDI-GAVNQNPF 359
Qy 360 SCSTFPLPLTPFVRSWLDGSDRGVAVTNMQTESFESTLGLRCGAFARAGSNVFPD 419
Db 361 NCNTISPLSTSPFVRIWLDGSDRGVAVTNMQTESFESTLGLRCGAFARAGSNVYPG 420
Qy 420 YFIRNIGSVPLVYRNEDLRPLHYNEIRNIESPSGTGGARAYVSVHNNKNNIYAHEN 479
Db 421 YFIRNIGSVPLVYRNEDLRPLHYNEIRNIESPSGTGGARAYVSVHNNKNNIYAHEN 480
Qy 480 GTMHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGQSDLRPEOSNTTAYTLRGNG 539
Db 481 GTMHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGQSDLRPEOSNTTAYTLRGNG 540
Qy 540 NSYNLYRVSSLGNSITRTINGRYTASNTTTNDGVNDGNARFLDINMGNYVASDN 599
Db 541 NSYNLYRVSSLGNSITRTINGRYTASNTTTNDGVNDGNARFLDINMGNYVASDN 600
Qy 600 TNPPLDINTVNSGTQFPELMNIMFVPTNLPY 632
Db 601 SDVPLDINTVNSGTQFPELMNIMFVPTNLPY 633

```

RESULT 10
US-09-041-991a-6
Sequence 6, Application US/09041991A
Patent No. 6107278
GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
Narva, Kenneth E.
Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida

```

COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,991A
FILING DATE: 13-MAR-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-709
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 623 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-041-991A-6

Query Match      78.8%; Score 2610.5; DB 3; Length 623;
Best Local Similarity 80.3%; Pred. No. 5.2e-224;
Matches 508; Conservative 46; Mismatches 68; Indels 11; Gaps 6;

QY 1 MNNVINGRTTCDAYNVVADHPSPFEHKSGLDTIRKEMWERTDHSLYVAPIVGVTSF 60
DB 1 MNNVINGSGNTTCHANNVADHPSPFEHKSGLNTIRKEMWERTDHSLYVAPIVGVTSF 60
QY 61 LKRVGSLIGKRILSELMLGIFPSGSTNLMODIRETEOPFNORLNTTLARVALEGL 120
DB 61 LKRVGSLIGKRILSELONLIFPSGSTIDLMOEILRATEGFINRNLADTLGRVNAELGL 120
QY 121 QANIRENOVDNFINPQNPVPLSTSSVNTMOQLFNLPOFRVQGYQLLLPLFAQA 180
DB 121 QANVAEENQVDNFINPQNPVPLAIDSVNTLOQLFSLRPLQGYQLLLPLFAQA 180
QY 181 ANMLSFIRVDVNLNADDEMGISAATLRTYONVLYKNTTESNYCINTYOTAFRGALNRLHD 240
DB 181 ANMLSFIRVDVNLNADDEMGISAATVTRDHLNFRDYSNVCINTYOTAFRGALNRLHD 240
QY 241 MLEFRTYMLNVEFYVSIWLSFKYOSLIVSSGANLYASGSGP--TOSFTAHNMPFLYSLF 298
DB 241 MLEFRTYMLNVEFYVSIWLSFKYOSLIVSSGANLYASGSGP--TOSFTAHNMPFLYSLF 298
QY 301 QVNSVYVINGSGARLTOTFPNIGLPGTTTTALAAAVNYSGVSGDVG--AVFNQNF 359
DB 301 QVNSVYVINGSGARLTITFNSNIGLPGSTTTOTLHFAIRINRGVSSRLGQANLNQNF 358
QY 359 NISTFLPNLQPTFKLSWLSGDRGVAITSNWOSGAFETTL--LFTSIFSRKGSNPFBD 417
DB 359 NISTFLPNLQPTFKLSWLSGDRGVAITSNWOSGAFETTL--LFTSIFSRKGSNPFBD 417
QY 420 YFIRNIGSVPLVWNEDELRRPLHVEIRNIESPSTPGGLRAYVSVNRRKNIIYAVHN 479
DB 420 YFIRNIGSVVGTISNADLRLPLHFEIRDI---GTTA--VASLTVANRRKNIIDYTHN 471
QY 480 GMTMILAPEDYTGFTLSPHATOVNNQRTISKRGNGDGLAREGSNTTARTLRNG 539
DB 480 GMTMILAPEDYTGFTLSPHATOVNNQRTISKRGNGDGLAREGSNTTARTLRNG 539
QY 472 GMTMILAPNDYTGFTLSPHATOVNNQRTISKRGNGDGLAREGSNTTARTLRNG 531
DB 472 GMTMILAPNDYTGFTLSPHATOVNNQRTISKRGNGDGLAREGSNTTARTLRNG 531
QY 540 NSINLYLVSSGLNSTIRVINGRYTASVNTTNNQDNGNGARFLDINMGVVASDN 599
DB 540 NSINLYLVSSGLNSTIRVINGRYTASVNTTNNQDNGNGARFLDINMGVVASDN 599
QY 532 NSYNLYLVSSIGSSTIRVINGRYTAA--NNTLTNNQDVLNNGARFSDINIGVVASAN 590
DB 532 NSYNLYLVSSIGSSTIRVINGRYTAA--NNTLTNNQDVLNNGARFSDINIGVVASAN 590
QY 600 TNPPLDINVTENSGTOPELMNIMFPTNLPPIY 632
DB 600 TNPPLDINVTENSGTOPELMNIMFPTNLPPIY 632

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Db 591 TNPPLDINVTENSGTOPELMNIMFPTNLPPIY 623

RESULT 11

US-09-608-533A-6
Sequence 6, Application US/09608533A
Patent No. 6534644

GENERAL INFORMATION:

APPLICANT: Schnepf, H. Ernest
Narva, Kenneth E.

Muller-Cohn, Judy

TITLE OF INVENTION: Toxins Active Against Pests

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: Florida

COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/608,533A

FILING DATE: 30-Jun-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/041,991

FILING DATE: 13-MARCH-1998

ATTORNEY/AGENT INFORMATION:

NAME: Sanders, Jay M.

REGISTRATION NUMBER: 39,355

REFERENCE/DOCKET NUMBER: MA-709D1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (352) 375-8100

TELEFAX: (352) 372-5800

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 623 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-608-533A-6

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Query Match      78.8%; Score 2610.5; DB 4; Length 623;
Best Local Similarity 80.3%; Pred. No. 5.2e-224;
Matches 508; Conservative 46; Mismatches 68; Indels 11; Gaps 6;

QY 1 MNNVINGRTTCDAYNVVADHPSPFEHKSGLDTIRKEMWERTDHSLYVAPIVGVTSF 60
DB 1 MNNVINGSGNTTCHANNVADHPSPFEHKSGLNTIRKEMWERTDHSLYVAPIVGVTSF 60
QY 61 LKRVGSLIGKRILSELMLGIFPSGSTNLMODIRETEOPFNORLNTTLARVALEGL 120
DB 61 LKRVGSLIGKRILSELONLIFPSGSTIDLMOEILRATEGFINRNLADTLGRVNAELGL 120
QY 121 QANIRENOVDNFINPQNPVPLSTSSVNTMOQLFNLPOFRVQGYQLLLPLFAQA 180
DB 121 QANVAEENQVDNFINPQNPVPLAIDSVNTLOQLFSLRPLQGYQLLLPLFAQA 180
QY 181 ANMLSFIRVDVNLNADDEMGISAATLRTYONVLYKNTTESNYCINTYOTAFRGALNRLHD 240
DB 181 ANMLSFIRVDVNLNADDEMGISAATVTRDHLNFRDYSNVCINTYOTAFRGALNRLHD 240
QY 241 MLEFRTYMLNVEFYVSIWLSFKYOSLIVSSGANLYASGSGP--TOSFTAHNMPFLYSLF 298
DB 241 MLEFRTYMLNVEFYVSIWLSFKYOSLIVSSGANLYASGSGP--TOSFTAHNMPFLYSLF 298

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QY 301 QVNSNYLNGFSGARLITOTFPNIGLPGTTTHALLARUNYSGVSGDIG-AVENONE 359
 DB 299 QVNSNYLNGFSGARLITOTFPNIGLPGTTTHALLARUNYSGVSGDIG-AVENONE 358
 QY 360 SCSTFLPPLTFEVRSMWLDGSDRGVNTVMQTESFEFTLGRCAFTARGNSNFPD 419
 DB 359 NISTLNPLOTFIRSMWLDGSDRGVNTVMQTESFEFTLGRCAFTARGNSNFPD 417
 QY 420 YFIRNIGVPLVVRNEDLRPLAYNEIRNIESPGTGGALAYVSNHRKNITVAHEN 479
 DB 418 YFIRNIGVPLVVRNEDLRPLAYNEIRNIESPGTGGALAYVSNHRKNITVAHEN 471
 QY 480 GTMTHLAPEDYGTFTSPHATOVNNQTRTFISEKGNQDGLRFEQSNTARTYTLRNG 539
 DB 472 GTMTHLAPEDYGTFTSPHATOVNNQTRTFISEKGNQDGLRFEQSNTARTYTLRNG 531
 QY 540 NSYLYRYSLSGNSTIRVTINGRVYASVNTTNNQVNDGNARPLDINGNVYASDN 599
 DB 532 NSYLYRYSLSGNSTIRVTINGRVYASVNTTNNQVNDGNARPLDINGNVYASDN 590
 QY 600 TNPVDINVTNFGTQFELANIMFVPTNLPPIY 632
 DB 591 TNPVDINVTNFGTQFELANIMFVPTNLPPIY 623

RESULT 12
 US-09-408-820-2
 ; Sequence 2, Application US/0940820
 ; Patent No. 6204057
 ; GENERAL INFORMATION:
 ; APPLICANT: Schmetter, Wolfgang
 ; APPLICANT: Krieger, Lutz
 ; APPLICANT: Zhang, Jiaming
 ; TITLE OF INVENTION: Polynucleotides And The Proteins Encoded Thereby,
 ; FILE REFERENCE: S-30403/A/OHD/CGC1996/PCT
 ; CURRENT APPLICATION NUMBER: US/09/408.820
 ; EARLIER FILING DATE: 1999-09-29
 ; EARLIER APPLICATION NUMBER: 09/051.454
 ; EARLIER FILING DATE: 1998-04-07
 ; EARLIER APPLICATION NUMBER: DE 195 40 223.5
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 706
 ; TYPE: PRT
 ; ORGANISM: Bacillus popilliae
 ; FEATURE:
 ; OTHER INFORMATION: strain subspecies: melolonthae H1; stage of
 ; OTHER INFORMATION: development: spore stage; cell type: sporangium
 ; FEATURE:
 ; OTHER INFORMATION: immediate origin: isolate from the haemolymph of
 ; OTHER INFORMATION: Melolontha melolontha individuals captured on open
 ; OTHER INFORMATION: ground
 ; FEATURE:
 ; NAME/KEY: PEPTIDE
 ; LOCATION: (1)..(706)
 ; OTHER INFORMATION: mature protein crystal peptide determined by
 ; OTHER INFORMATION: experiment
 ; US-09-408-820-2

Query Match 32.6%; Score 1080; DB 3; Length 706;
 Best Local Similarity 38.4%; Pred. No. 1.7e-87;
 Matches 264; Conservative 96; Mismatches 233; Indels 94; Gaps 21;
 QY 2 NNVNAN-----GRITICDA-----NVVADHPSEFKSLDTIRKEMWKRFD 45
 DB 58 NNDNNDAICDELGTPIIDNNTICSTDPFINVARDP--FKKSTQELIRKEMWKRFD 115
 QY 46 HSLVYAPVGVSSFLIKKVGSLIGKRLISEMGLIFPESGNNLMQDILRETFQPLNQL 105
 DB 116 PSILTPAIVGVVTSFLQSLIKQKATSPFLIKTLTDLLEPNNSSLTWEILRATBOYQERL 175

QY 106 NDTPLARVNAELFEGLOANIREFNOQVDFNLPONVPLSTSSVNTMOQLFLNRLPQR 165
 DB 176 DIDTANRVSQGLVGLKNLTTFNDDVEDFQNRNGISPLAIDSINTMOQLFVNRLPQR 235
 QY 166 VOGYQLLPLFPAQANMHLSPTRVYVLANDENGICSAATLFRQYVLYKNNTYSNYCN 225
 DB 236 VSGYQVLLPLFPAQANMHLSPTRVYVLANDENGICSAATLFRQYVLYKNNTYSNYCN 295
 QY 226 TYQAFRGANTR-----LHMLERFTYMFANVEVYSIWSLFKYQSLVYSGANDYASG 279
 DB 296 TYQDGR---TRFPRNTLEDMLQFKTEFMTNALDIVSISMLKYNLYSTANLYNIG 352
 QY 280 SGPQQTQSTQDMPELYSLPQVNSNYLNGFSGARLITOTFPNIG-----LPQTTTH 333
 DB 353 DNKMEGAYPISYGPFPNSYIQTKNVYVLSGVSGIGARFYSTVIGRYLHDLKNITTT 411
 QY 334 ALTAARVNSGVSAGDYGAVFN-----QNFSCSTFLP-PLLRP 371
 DB 412 -----YGGTGQPIGVQSLTTELDLKKQQAATBDSLVDPQFFTLNCLMFPNITAP 463
 QY 372 -FVRSMLDSG-SDRGVNTVMQTESFEFTLGRCAFTARGNSNFPDYFIRNIGV 428
 DB 464 YFATSLYSESRYSIGYLRKOVKES--DSTGGLNPAWTS-----YDYITNHSAT 515
 QY 429 PLVVRNEDLRPLAYNEIRNIESPGTGGALAYVSNHRKNITVAHENGTMHLAP 488
 DB 516 VQINGENTDTTPLYFKNRPITSRGV---NKVAVYVRKANIAGTNGMTIHQADP 570
 QY 489 DYGTFTSPHATOVNNQTRTFISEKGNQDGLRFEQSNTARTYTLRNG-NSNYLYR 547
 DB 571 DGTGFTVSPHPSA--NTTYSIKENYVSGSLHL-KGGTILHMLGNGQDPTRYLAR 627
 QY 548 VSLGNSITIRVTINGRVYASVNTTNNQVNDGNARPLDINGNVYASDNVVD 605
 DB 628 LSGAN---QWLGSPFTSYAFDSTINNEGITNGSKFQPAFSTPVIDEOK-----E 679
 QY 606 INTFNSGTQFELANIMFVPTNLPPIY 632
 DB 680 IIVFPGVGSJLMMNLFLPADDTPLY 706

RESULT 13
 US-08-793-331-7
 ; Sequence 7, Application US/0879331
 ; Patent No. 6071877
 ; GENERAL INFORMATION:
 ; APPLICANT: DEBCLUSE, ARMELE
 ; APPLICANT: THIERY, ISABELLE
 ; TITLE OF INVENTION: NEW POLYPEPTIDES HAVING A TOXIC ACTIVITY AGAINST
 ; FILE REFERENCE: 0660-0116-0 PCT
 ; CURRENT APPLICATION NUMBER: US/08/793,331
 ; EARLIER FILING DATE: 1997-05-13
 ; EARLIER APPLICATION NUMBER: PCT/FR95/01116
 ; EARLIER FILING DATE: 1995-08-24
 ; EARLIER APPLICATION NUMBER: FR 94/10299
 ; EARLIER FILING DATE: 1994-08-25
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 644
 ; TYPE: PRT
 ; ORGANISM: B. thuringiensis ser. israelensis
 ; US-08-793-331-7

Query Match 10.2%; Score 336.5; DB 3; Length 644;
 Best Local Similarity 23.1%; Pred. No. 2.7e-21;
 Matches 167; Conservative 98; Mismatches 257; Indels 201; Gaps 34;
 QY 27 EHSKSLDTIRKEMWKRFDLSLY-----VAP---YGVVSSFLIKKVGSLIGKRLISE 76
 DB 3 EDSKSLDTLSIV---NETDFPLNNYNTTEFTIPALINAVPAQIYLAFTALCKKAAKAAFSK 58

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QY 77 LMGILPSSGNTLMODILRETEQFINQRIINTTLARVNALEGLQANIREFNOQVNL- 135
DB 59 VLSILPFGSQPATMEKVEVETLLINQKLSQDRVILNABRG-----LIEVSDFPDYIK 114
QY 136 NPTQNVPLSTISSVNMQOLFLN-----RLPQVQYQYLLLEPFAQANMLSFT 188
DB 115 QPQFTPA-----TAKGYFLNLSGAILIQLPQFEVQYQYBSVSLAFTQWCTLAHTLL 165
QY 189 RDVVLNADWGISAAATLRTYQNYLKNYTESNYCINTYQTA-REGNTRILMDLSEPRY 247
DB 166 KDGIILAGSAMGFTQADVDSPFLKFNQKVDARTILMMEYERGLCKVSLKDLGTRKMK 225
QY 248 MFLNVEYVSIWLSFKYOSLLVSSGANLYASSGPQOTQSFISQWPLYSLLFOVNSN- 305
DB 226 CNLYVPPRANSLMRFBGLKQSSLSL-----MDVYGVSIYVNNEM 268
QY 306 ----YVINGPSGARLTQTFPNIGLPGTTTHALLAARVNSG-----GVSSGDIGAVF 355
DB 269 GGLVYKLLMGEVNOBLTTFVKNY-----SFTNEPADIPARENIRGVHPIYDSSGLTWIG 324
QY 356 N---QNFSCSTFLPPLTPPVRSWLDSDGQVNTYTNQ----- 393
DB 325 NGRTNENPAD-----NNGNEIMEVRTQTFYQNPNEPIAPEDIIINOILTA 370
QY 394 ----TESFESTL---GLRCGAFARGN-----SNY--FPDYFIRAI 425
DB 371 PABADLFFRNADINWKFQFOSLYGNWIKLQTVLSSRTGTLPRNYLAHYGYIRAI 430
QY 426 SGVPLVVR---NEDLRPPHLYNEINIESPSG-----TPGLAAVNSVNRKNNTYA 475
DB 431 SACPQSVLAINHDL-TTLTYNRI-EYDSPTEIIVGAPNNTQF-----YSKKS- 480
QY 476 VHENGTMIHAPEDYGTFTISPIHATOVNNTFTISEKFGNOGD-SUREQOS--NTTAR 532
DB 481 ----HYLSETNDSYIIPALOPAEVSD--SSFLQDPDQATGSIKFAFPFISNEAK 530
QY 533 YTLRGNGNSYNLYLAVSSIGNSTIIVTINGSVYTAENVTTNNQVNDGAFPLDING 592
DB 531 YSIRLN-TGFYATARKYL-----IKVRVPTYL-PACIVQNSGNN-----RMLGSPFA 579
QY 593 NV-----VASDNTVPLDINV-TFNSGTQFELMINIMFV-----PTNL 628
DB 580 NNPBWVDFTTADFTNDLGITTSNALPSISSDSISGEMWOLFLVKSAPFTOI 639
QY 629 PPI 631
DB 640 NPL 642

```

RESULT 14
US-08-286-870A-4

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; Sequence 4, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLANK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286, 870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 648 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-286-870A-4

Query Match 9.9%; Score 327.5; DB 3; Length 648;
Best Local Similarity 22.8%; Pred. No. 1.7e-20;
Matches 162; Conservative 103; Mismatches 271; Indels 173; Gaps 32;

QY 21 HDPSFEHK-----SLDTIRKEM-MEMKRDH-----SLY--VAP----- 52
DB 9 HQSSSNAXKXDKSISLSKMETDELONINHEDCAKSEYNEVFPFASSTQGTIGTAG 68
QY 53 -IVGVSSFLKKVQSLGKILSELMGLFPSSGNTLMODILRETEQFINQRIINTDTIA 111
DB 69 KILDTGLVPPAQVASLY-SFLIGELM---PRGR-NQMEIFMEHBEILINOKISTYARN 122
QY 112 RVNAELGLQANIREFNOQVNDPFLNPTQNPVPLSIT-SSVNIQOOLFLNRLEPQVQYQ 170
DB 123 KALTDLKGGLDALVAYHDSLESWGRNNTRARASVYSQYLAELMFVQKLSFVSGSE 182
QY 171 LLLPLPFAQANMLSFTRDVVLNADWGISAAATLRTYQNYLKNYTESNYCINTYQTA 230
DB 183 VLLPPIYADANMLHLLLRDASIFGKMGWSSSEISTFYNRQVERADGSDHCWVSTG 242
QY 231 FRGL-NTRLHDL-----EFTYMEFLNVEYVSIWLSFKYOSLLVSSGANL---YASGSP 282
DB 243 LNNLRGTNAESWVRVYQFRDMTLVLDVALFPDYDQWYPIKTRQULREVTDAIGT 302
QY 283 QQQO-SFTSODW-----PFL-----YSLFOVNSN-YVINGPSG 313
DB 303 VHPHPSFTSTWYNNNAPSALAAVAVENPHLDPLEQYTTISLSRWSNTQVNNMGG 362
QY 314 ARLTQTFPNIGLPGTTTHALLAARVNSGGVSSGDIGAVNFQNSCTFLPPLTPPV 373
DB 363 HKL-EFTTIGTINISF-----QSTNTGAINVTLPFT 394
QY 374 RSWLDGSDRGQVNTV-----NMQ--TESFESTLGLRCGAFARGNSTFPD 419
DB 395 SRDYVTSBLAGLNLFTQVNGVNPVDFHMKFVTHDIA-----DNFYFG 441
QY 420 YFRNITSGVPLVVRNEDLRPPHLYNEINIESPSGTGGLRAVNSVNRKNNTYA-VHR 478
DB 442 Y-----AGIGQLODSNELPPEATQOPVYESYHRLSHIG-LTASHVYALVYSWTRH 494
QY 479 NGTMIHAPEDYGTFTISPIHATOV-----NNGTRFTISEKFG-NOGDSLRFGQSTTA 531
DB 495 SA-----DRTN-TIEPNSITQIFPKAFNLSGAAVVRGEGTGADILR-KTWTGT 543
QY 532 RYLRNGN-----SYLYLAVSSIGNSTIIVTINGSVYTAENVTTNNQVNDGANGARF 586

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Fri Aug 15 11:51:34 2003

us-10-040-906a-2.rat

Page 10

Db 544 FGDIVNINPPFAORVIRIRVASTTDLQFTSINGKAINQNFSAITNR-----GRD 596
QY 587 LIDINGNVVASDNTNVDLINTV-----FNSGTQFELMNTMFPVPTL 628
Db 597 LDYKTRTVGFTTFFSLDVOSTFTTIGAMNFSGNEVYIDRIEFPVEV 645

RESULT 15
US-08-286-870A-8
Sequence 8, Application US/08286870A
GENERAL INFORMATION:
PATENT NO. 6063605
APPLICANT: ELY, S
APPLICANT: TAILOR, RH
APPLICANT: BLENK, RG
APPLICANT: TIPPETT, JM
TITLE OF INVENTION: BACTERIAL GENES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CUSHMAN DABRY & CUSHMAN
ADDRESSEE: Intellectual Property Group of
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,870A
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520228
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8910624.9
FILING DATE: 09-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: PAUL N. KOKULIS
REGISTRATION NUMBER: 16, 773
REFERENCE/DOCKET NUMBER: 70608/220720
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 719 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-870A-8

Query Match 9.9%; Score 327.5; DB 3; Length 719;
Best Local Similarity 22.8%; Pred. No. 2e-20;
Matches 162; Conservative 103; Mismatches 271; Indels 173; Gaps 32;

QY 21 HDPSFEHK---SLDTIRKEW-MEMKATDH-----SLY-VAP-----52
Db 9 HOSFSSNAKVDKISTSLKNEETDILQINHEDECLMSSEYENVEPVSASTIQTGIGAG 68
QY 53 -IVGVSSFLKKVSGISGRILISELMGLIFPSGSTNLNODILRETOQFNLQRLNTDTLA 111
Db 69 KILGLSVPRFAGVASY-SFLIGELW-----PKGK-NQWEIPEHVEEIIINOKISTYAN 122
QY 112 RVNALEBGLQNTRENOQVDFLNPONPVPLST-SSVNTMOQLNRLNPOFRVQGY 170
Db 123 KALTDLKGIDALAVVHDSLESVGNRRNTRARSVKSQYIALEIMFVOKLPSFVSGEE 182

QY 171 LIALPLFAOANMHLSPIRDVVLNADSKGISATLRTYQNTLKNVTTETYSNYCINTYQTA 230
Db 183 VDLPLPIAQAANLHLLLRDASIRGKEMGSSSEISTYNNQVBRAGDYSDHCVMKSTG 242
QY 231 PRGL-NTRLHDL---ERRTYFLANVEEYYSIMSJPKQSLVSSGANI-----VASGSGP 282
Db 243 LNNLRGTNASWVRXVQFRDMTLMVLVLPSPSIDYQMPKITTKQLTREVYDAGT 302
QY 283 OCTQ-SFTSQDW-----PFL-----YSLFQVNSN-YVLNGFSG 313
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QY 314 ARLVTPPNIGLPGITTHALLAARVNSGVSSGDDGAVFNQNFSCSTFLPLTPEV 373
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QY 374 RSMIDSGSDRGVNTV-----NMQ--TESPSTLGRGCAFTARKNSNYFPD 419
Db 395 SRDVYRTESLAGNLFLTPVNGVPRVDFPMKPVTHPIAS-----DNFTYFG 441
QY 420 YPRNIGSVPLVRENEDLRLPHVNEIRNIESPGTGGILAAVNSVHNRKNNIYA-VHE 478
Db 442 Y----AGIGTQODESENEPPEATGQPNYESYHLSHG--LISAHVKALVSWTHR 494
QY 479 NGTMHLAPEDYGTISPPIHATQV-----NNQRTFISEKFG-NQDGLREQSNTTA 531
Db 495 SA-----DRTN-TIEPNSITQIPVKAENLSGAAVVRGPGTGADILR--RTNIGT 543
QY 532 RYTLRGNGN-----SYNLVLRVSSLSGNTIRITINGRVYLTASNVTNNNDGVNDGARF 586
Db 544 FGDIVNINPPFAORVIRIRVASTTDLQFTSINGKAINQNFSAITNR-----GRD 596
QY 587 LIDINGNVVASDNTNVDLINTV-----FNSGTQFELMNTMFPVPTL 628
Db 597 LDYKTRTVGFTTFFSLDVOSTFTTIGAMNFSGNEVYIDRIEFPVEV 645

Search completed: August 14, 2003, 18:13:21
Job time : 32 secs

Fri Aug 15 11:51:35 2003

us-10-040-906a-2.rapb

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 14, 2003, 18:11:07 ; Search time 28 Seconds
(without alignments)
2956.931 Million cell updates/sec

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Sequence: 1 MNVIVNNGRTICDAHVVA.....GTQELMNTMPTLPTPY 632

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Gapop 10.0 , Gapext 0.5

Searched: 492763 seqs, 131003257 residues

Total number of hits satisfying chosen parameters: 492763

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
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2: /cgn2_6/ptodata/1/pubpaa/FCI_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	311.5	9.4	1156	US-10-099-285-72	Sequence 72, Appl
2	305.5	9.2	643	US-09-826-660-25	Sequence 25, Appl
3	305.5	9.2	1186	US-09-826-660-23	Sequence 23, Appl
4	275.5	8.3	1207	US-09-988-462-7	Sequence 7, Appl
5	272	8.2	1177	US-10-035-060-6	Sequence 6, Appl
6	269.5	8.1	667	US-10-032-717-8	Sequence 8, Appl
7	269.5	8.1	673	US-10-032-717-18	Sequence 18, Appl
8	269.5	8.1	1210	US-10-032-717-4	Sequence 4, Appl
9	268	8.1	1155	US-09-756-643-2	Sequence 9, Appl
10	268	8.1	1155	US-09-988-462-9	Sequence 9, Appl
11	268	8.1	1181	US-09-988-462-11	Sequence 11, Appl
12	268	8.1	1181	US-09-988-462-13	Sequence 13, Appl
13	268	8.1	1181	US-09-988-462-15	Sequence 15, Appl
14	268	8.1	1181	US-09-988-462-17	Sequence 17, Appl
15	268	8.1	1181	US-09-988-462-28	Sequence 28, Appl

16	267.5	8.1	1178	9	US-09-851-194-2	Sequence 2, Appl
17	266	8.0	1177	15	US-10-035-060-2	Sequence 4, Appl
18	265	8.0	605	9	US-09-826-660-4	Sequence 2, Appl
19	265	8.0	1148	9	US-09-826-660-2	Sequence 6, Appl
20	265	8.0	1174	9	US-09-826-660-6	Sequence 8, Appl
21	265	8.0	1177	9	US-09-873-873-34	Sequence 34, Appl
22	264	8.0	1177	15	US-10-035-060-8	Sequence 4, Appl
23	264	8.0	1179	15	US-10-035-060-8	Sequence 4, Appl
24	263	7.9	617	14	US-10-032-717-34	Sequence 34, Appl
25	263	7.9	670	14	US-10-032-717-24	Sequence 24, Appl
26	262.5	7.9	1177	9	US-09-873-873-28	Sequence 28, Appl
27	262.5	7.9	1177	11	US-09-997-914-28	Sequence 28, Appl
28	262	7.9	617	14	US-10-032-717-46	Sequence 46, Appl
29	262	7.9	670	14	US-10-032-717-44	Sequence 44, Appl
30	261.5	7.9	620	14	US-10-032-717-32	Sequence 32, Appl
31	261.5	7.9	673	14	US-10-032-717-22	Sequence 22, Appl
32	261.5	7.9	1156	9	US-09-826-660-15	Sequence 15, Appl
33	261.5	7.9	1177	9	US-09-873-873-26	Sequence 26, Appl
34	261.5	7.9	1177	11	US-09-997-914-26	Sequence 26, Appl
35	260.5	7.9	620	14	US-10-032-717-42	Sequence 42, Appl
36	260.5	7.9	673	14	US-10-032-717-40	Sequence 40, Appl
37	260.5	7.9	1163	9	US-09-756-526A-2	Sequence 2, Appl
38	260.5	7.9	1163	12	US-10-345-020-2	Sequence 2, Appl
39	260.5	7.9	1177	9	US-09-873-873-10	Sequence 10, Appl
40	260.5	7.9	1177	9	US-09-873-873-12	Sequence 12, Appl
41	260.5	7.9	1177	9	US-09-873-873-14	Sequence 14, Appl
42	260.5	7.9	1177	11	US-09-997-914-10	Sequence 10, Appl
43	260.5	7.9	1177	11	US-09-997-914-12	Sequence 12, Appl
44	260.5	7.9	1177	11	US-09-997-914-14	Sequence 14, Appl
45	258.5	7.8	616	14	US-10-032-717-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-10-099-285-72
; Sequence 72, Application US/10099285
; Publication No. US20030105319A1
; GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
Wicker, Carol
Narva, Kenneth E.
Walz, Michelle
Stochoff, Brian
Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/099,285
FILING DATE: 15-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/002,285
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/866,615
FILING DATE: 1-JUN-1997
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.

REGISTRATION NUMBER: 39,355
 REFERENCE/DOCKET NUMBER: MA-701C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (352) 375-8100
 TELEFAX: (352) 372-5800
 INFORMATION FOR SEQ ID NO: 72:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1156 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 72:
 US-10-099-285-72

Query Match 9.4%; Score 311.5; DB 15; Length 1156;
 Best Local Similarity 23.3%; Pred. No. 3.5e-19;
 Matches 157; Conservative 96; Mismatches 221; Indels 199; Gaps 32;

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 87 PFGQIVSFY-----QFLNTLM-----PNDTALWEAKRQVELNMOITEFARN 133
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 168 GVQLLLPLPAQANMELSFIRDVVLNADKWSIAATRTQNTLYKNTTESNYCINTY 227
 191 GQVPLLSVVAQAVNHLLKLDASLGEEMGTFQGEISTYDQLELTKNTNCEWY 250
 228 QYA---FRGLNT---RLHMLFETVFLNVEEYISWSLFRKQSLVSSGANLYASGS 280
 251 NIGDLRLKGTNTESMRLYH---QFRREMTLVLDV---ALFPYDV-----RLYPTGS 298
 281 GPOQTOS-FTS-----QDW-----PFLY-----S 298
 299 NQILREYVYDPIVENPPANVGLCRWGTNPNTFSELENAPIRPPLFRLNLSLTSSN 358
 299 LFOVNSNYLNGFSGARLTQTPNIGLPG-----TTTTHLLAARVNSGGVSSGDIG- 352
 359 REPVSNNF-MDYSGHTLRSLANDSAVQEDSYGLITTRATINPGVDGNRIESTAVDF 417
 353 ----AVNQNFGSCFTLEPLLPVYSMLDSSD---RGQNTV---TMMQTESBESTIG 402
 418 RSALIGLYGVN-----RASVFGGLFNGTISPNANGSGRDLYDINDELPPDEST- 465
 403 LRCAFTARGNSNYPDY-----FIRNISGVPLVY---RNEDLRRLPHAYNEIRNIESPS 453
 466 ---GSGTHRLSHVTFFSPOTNOAGSIANAGSVPTVYWRDRVDVNTITFNRIITQLP- 519
 454 GTPGGLRAYMVSYANKNNIYAVHENGTMHLAPEDYGTFTISPIHATQVNNQTRTFISE 513
 520 -----LVKA-----SAPVSGITVYKGP-----GFT----- 539
 514 KFGNQGDSLRPEQSNLTARTYLRGNNS-----YNLYRVSSLGSTIRTINGRVYAS 568
 540 ---GGILRTTNGTFC--TLRYTVNSPLQRVRYRFASSGNFIRI-LRGNSTIAY 592
 569 NVAITTNNDGVNDNGARFLDIMGVVASDNTVPLDINVT-----NSGT 614
 593 QRFSGTNRG-----QELTVESFTVSEFTTNOGLPFTTQAOENLTITLAEGVSTGS 644
 615 QELNMINIMEPTN 627
 645 EYFIDRIEILPVN 657

RESULT 2
 US-09-826-660-25
 Sequence 25, Application US/09826660
 Patent No. US20010026940A1
 GENERAL INFORMATION:

APPLICANT: Cardineau, Guy A.
 APPLICANT: Stelman, Steven J.
 APPLICANT: Narva, Kenneth E.
 TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
 FILE REFERENCE: MA-714X2D1
 CURRENT APPLICATION NUMBER: US/09/826,660
 PRIOR FILING DATE: 2001-04-05
 PRIOR APPLICATION NUMBER: 09/178,252
 PRIOR FILING DATE: 1998-10-23
 PRIOR APPLICATION NUMBER: 60/065,215
 PRIOR FILING DATE: 1997-11-12
 PRIOR APPLICATION NUMBER: 60/076,445
 PRIOR FILING DATE: 1998-03-02
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO 25
 LENGTH: 643
 TYPE: PRT
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
 US-09-826-660-25

Query Match 9.2%; Score 305.5; DB 9; Length 643;
 Best Local Similarity 22.5%; Pred. No. 5e-19;
 Matches 142; Conservative 101; Mismatches 265; Indels 123; Gaps 25;

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 171 LLLPLPAQANMELSFIRDVVLNADKWSIAATRTQNTLYKNTTESNYCINTYOTA 230
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 221 FRGL-NTRLHML---ERTVFLNVEEYISWSLFRKQSLVSSGANLYASGSGE 282
 229 LNNIRGTNMSWLRNFRDRLTGLVLDVALLFPSYDTRVYPMNTSADLTREITDPIGR 298
 283 QOQTOS-FTSQDMPFLYSLFOVNSNYLNGFSGARLTQTP-FNIGLPGTTTTHLLAARV 340
 299 TNAISGFEASTM-----FNNN--ABSFALIEAVIRPPLHDPBQTLTFSVLSRMS 348
 341 NYSGVSSGDIGAVNQNFGSCFTLEPLLPVYSW---LDSGSRGVNTVN----- 391
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 392 -----WQTESFES-----TLGLRCAFTARGNSNYPDYFIRNI--SG 427
 381 SINVTLLQFTSRDVRIBESFAGINILLTPVNGVPMARFWMRPNLSLRGSLTYIGYTS 440
 428 VPLVWRENDRLPLHAYNEIRNIESPBGCGCLRAYMVSYANKNNIYA-VHENGTMHLA 486
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 493 --DRTN-TISSDSITQILPVKSPNLNSGTSVSGFGTGDILRTVNGSVLSMGLFNN 549
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 610 SSGST---AGISISNNAQRQTFHDKIEFTP 637

RESULT 3

US-09-826-660-23
Sequence 23, Application US/09826660
Patent No. US20010026940A1
GENERAL INFORMATION:
APPLICANT: Cardineau, Guy A.
APPLICANT: Stelman, Steven J.
APPLICANT: Narva, Kenneth E.
TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
FILE REFERENCE: WA-714XC2D1
CURRENT APPLICATION NUMBER: US/09/826,660
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/1178,252
PRIOR FILING DATE: 1998-10-23
PRIOR APPLICATION NUMBER: 60/065,215
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/076,445
PRIOR FILING DATE: 1998-03-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
LENGTH: 1186
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-23

Query Match 9.2%; Score 305.5; DB 9; Length 1186;
Best Local Similarity 22.5%; Pred. No. 1,3e-18;
Matches 142; Conservative 101; Mismatches 265; Indels 123; Gaps 25;

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73 PPAQGLASFSFLVG-----ELM-----PRG-RDPMELFLEHQLINQOITENRDR 118
112 RNVAELGLQANIRENQOVNFIPTQNPVPLSTSSVNTMOOL-FLNRLPOFRVQGY 170
119 TALARLQGLSFRAYQOGLSDWLENRDARRSVLYTYOYALDELFLNMLFAIRNOE 178
171 LLLPLPQANMHLSPFRDVLNDEMISATLRTYQYVLAQNTYSYCNINYQTA 230
179 VPLIMVYAOANLHLRLKASLFGSEFELTSQELQRYRQYREKRESDYCARWNTG 238
231 FRGL-NTRLHMDL--EERTYMLNFEVYSIWSLFFYQSLVSSGANL-----YASGSGP 282
239 LNNLRGTVAESWLRNQFRDLTLGLVDLVALFPSYDTRVYPMNTSAGLTREIYTPDGR 298
283 QQTQS-FTSQMPPFLYSLFQVNSNYVANGFSGARLTQTF-PNIGLPGTTTHALLANV 340
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441 VGTQLDSETELPEPETERENYVSHLSNIR--LISNLTARAVYSWTHRSA----- 492
487 PEDYGFITSPHATOVN-----NQRTRISKEKNQODSLREGSNTTARTIKRGNG 539
493 --DRTN--TISDSITQPLVYKSNLSGTSVSSGEGTGDIIRTVNAGVLSMGINFEVN 549
540 NS---YNLYRVSLSNGSTIRYVING-RVYASNVNTTTNNDGVANDGARELDINNGNV 595
550 TSLQRRVRYVYASQTMVLRVYVGGSTTFQCGPSTMSANSLTSGFRFAEPVYGISA 609
596 ASDNTNVPDLNVTENGSTQ-PELNNIMFVP 625

Db 610 SSGQT---AGISISNNAGRTFHFDKIEFIP 637

RESULT 4
US-09-988-462-7
Sequence 7, Application US/09988462
Publication No. US20030046726A1
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Marten, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Laudis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Syngenta Biotechnology, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-NOV-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:
NAME: Weigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8687
TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-988-462-7

Query Match 8.3%; Score 275.5; DB 11; Length 1207;
Best Local Similarity 21.9%; Pred. No. 7.4e-16;
Matches 152; Conservative 98; Mismatches 226; Indels 217; Gaps 33;

52 PIVGVTSFLKKVSLGKRIISLMLGIFPSGNTIMODILRETFQFLNRLNTDTLA 111
47 PPAQGLASFSFLVG-----ELM-----PRG-RDPMELFLEHQLINQOITENRDR 92
112 RNVAELGLQANIRENQOVNFIPTQNPVPLSTSSVNTMOOL-FLNRLPOFRVQGY 170
93 TALARLQGLSFRAYQOGLSDWLENRDARRSVLYTYOYALDELFLNMLFAIRNOE 152

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; PRIOR FILING DATE: 1986-09-05
; PRIOR APPLICATION NUMBER: US 06/808,129
; PRIOR FILING DATE: 1985-12-12
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent version 3.0
; SEQ ID NO 6
; LENGTH: 1177
; TYPE: PRF
; ORGANISM: Bacillus Thuringiensis
; US-10-035-060-6

Query Match      8.2%; Score 272; DB 15; Length 1177;
Best Local Similarity 22.6%; Pred. No. 1,5e-15;
Database 156; Conservative 100; Mismatches 272; Indels 170; Gaps 29;

QY 6 NNGRTTCDAVNVVADHPPEFEEKSLDTRKEMWEMKRT--DHSLYVAPVIGYVSSFLK 63
DB 3 NNNININEICPNICIS-----NPEVSVAGGRIRIETGYTIDISL-----SUTQPLS 48
QY 64 K----VSGILKRIELSELWGILPFPGSGTINMODILRETEOPFLNQRLNTDPLARVNALEEG 119
DB 49 EFPFAGGVGLG--LVDTIMGIFGSS-----QMAFLVYEQELQNLREEPARNQALSRLEG 102
QY 120 LQ-----ANIREPQOVNDFLNPOTNPPVPLSTSSVNTMGOQLFLANLPQFRVQGL 172
DB 103 LSLRLYOIVAEFPRME-----ADPTPALREEMKIQFNQMSALTTALPLFAVQNTQVP 156
QY 173 LLEPLFAQANNEHLSFIRDVLINADENGISAAITLFTYQVYKNTTEYSNYCINTYQTAER 232
DB 157 LLSVYQAAHHLSVLRDVSVCQRMGFDAATINRSYNDLTRLIGYTDVAVRWYGTGLE 216
QY 233 ----GANTRLHML--EERTYFNLNVEEYSIMSLFKXQSLVSSANLVASGSGPOOT 286
DB 217 RWVGPEPSR--QWARYNQFRELTLTVDIVALP-----NDSRRYPIRTY 260
QY 287 SFTSQDMPFLYSLFQVANSNYVLNFGSA-----RLTQFPNICGLPGTTT----- 332
DB 261 SOLTR-----EITPPLVLENFDFSGFRGSAOGIERISIRSHLMDIINSTITTYDAHR 311
QY 333 -----HALLAANVYSGGVSS-----GDIGAVFNQNSCSTFLPPLTFPFRSLMDSGS 381
DB 312 GIYYWSGHQIMASVGFSGPEFTPLPYKTMG-----NAAPQGIIVAQGGQVYTLSTSL 366
QY 382 DRGVNVTVNMQTESFESTLGLRGCAFTARQNSNTFEDYIFR-----NISGV-----L 430
DB 367 YRPPFPIGINNQ-----OLSLVDTGTEFAVGTSNMLPFAVYRKSCTVDSLNEIPPONNV 420
QY 431 VVNEEPLRLPHYNEIRNIESPCGTPGGLRAYVVSVAHRK--NNIYAVHE----- 478
DB 421 PPHQEFSHRLSHVBMRSFGSSSV--SITDAPFEMQHSMEFNINIIPSSQITQIPLTKS 479
QY 479 ---NQMIIHLAPEDYTGFTISPIHAQVNNQTRFISEKKGQSGSLAFBSNITARY 534
DB 480 TNLGSGTSVAGKP-----GFT-----GGDILR--RTSGQIST 510
QY 535 LRGN-----GNSYVLYLRSSLGKSTRTVINGRVYTAASNVTITNNDGVNDGARFLDI 589
DB 511 LRNNITAPLSGRYVVRIRASVITNLQCHTSTIDCRPLINGNSFATWS--GSNLQSGSRV 569
QY 590 NMGAVVASDNTNVPDLIN--TNSGTQFELMIMFPIYNL 628
DB 570 GFTTPFNFSGNSVFTLSAHVNSGNEEYVIDRIEVPALV 609

RESULT 6
US-10-032-717-8
; Sequence 8, Application US/10032717
; Publication No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Peng
; APPLICANT: Ronald D. Flanagan

```

```

; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins with
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (truncated)
US-10-032-717-8

```

```

Query Match      8.1%; Score 269.5; DB 14; Length 667;
Best Local Similarity 22.7%; Pred. No. 1e-15;
Matches 135; Conservative 91; Mismatches 221; Indels 147; Gaps 24;

```

```

QY 53 IYGVSSFL-LKKVSLIGKRIISLMGLIFPGSGTNLMODILRETEQFLNRLNDTTLA 111
DB 76 IYKLSLGLGVFPVPIVS--LYTQLDIDILPSSGQSQWEIFMEQVEELINOKIAEYARN 133
QY 112 RVNALEGLQANIREFNOQVDFL-NPTONPVLSTSSVNTMOQLFLNRLPQFRVOGYO 170
DB 134 KALSELBGLANNVQYLTLAEEMKENPNSRALRDVRNREILDSLFTQYMPSERYTNE 193
QY 171 LLLLEPFOAANMHSFRDVLNADENGISAATLTQYNTLAKNTTBYSNCTNYOTA 230
DB 194 VPELTVYQAAVHLHLLKODASIFGEWGSSTYINNYDRQMKLAEYSDHCCKVWEYG 253
QY 231 FPGIN---TLHDMLEFRTYMFANFEVYSIWSLFKYOSLIVSSGANL---YASGSGP 282
DB 254 LAKLGTSAKQWVDYNOFRSEMTLVLDVVALFPNDRTYRMYETKQLTREYTDPLGA 313
QY 283 QQTQSTQDMPFLXSLFQVNSNYVANGSGARLTOTFPNIGLPGTTTHALLAR--- 339
DB 314 VNVSSIGS--WYDKAPSFVIESSVY-----RPHVFDYITGLVYQSSISASARYR 365
QY 340 -----VNVSGVSSGDIGAVF--NONF--SCSTFLPLLPFRSWLSDSGDRGVNTVT 390
DB 366 HMAHQIISYHRIFSQDNIHKOMYGTQNLHSTF-----DPT 402
QY 391 N---WQTESFESTGLRCGAFTRKNSNTPEDY-FIRNISGV-----LYVRNEDLRRL 441
DB 403 NYDIYKTLKDAVL-----LDIVFPGYTYI--FPGMEVEFEPVWQNLNTRKTL 449
QY 442 HYNELR-----NIESPS-----GTPGGLRAYMVSVH 467
DB 450 KNPVSKDIIAGTRDSLELPETSQPNYBESYHRLCHITSIPAGSTGLGVVPSWTH 509
QY 468 NRKNNTYAVHENG-TMI-----HLAPF-----DYTGT-----ISPHTATVQNNQ 506
DB 510 RSDADLINAVHSDKITQIPVVKVSDLABSITGGPNNTVVSGBPFGGGLIKYIRNGVISH 569
QY 507 TETFLSEFGNQGDSLRFESQNTT-----ARYTL-RGNQNSYNYL 545
DB 570 MRYKISDINKEYSMRIRYASANNTEFYINPSEENVKSHAKTMNRGELTYNNK 623

```

```

RESULT 7
US-10-032-717-18
; Sequence 18, Application US/10032717
; Publication No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flammagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims

```

```

; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins with
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (truncated)
US-10-032-717-18

```

```

Query Match      8.1%; Score 269.5; DB 14; Length 673;
Best Local Similarity 22.7%; Pred. No. 1.1e-15;
Matches 135; Conservative 91; Mismatches 221; Indels 147; Gaps 24;

```

```

QY 53 IYGVSSFL-LKKVSLIGKRIISLMGLIFPGSGTNLMODILRETEQFLNRLNDTTLA 111
DB 76 IYKLSLGLGVFPVPIVS--LYTQLDIDILPSSGQSQWEIFMEQVEELINOKIAEYARN 133
QY 112 RVNALEGLQANIREFNOQVDFL-NPTONPVLSTSSVNTMOQLFLNRLPQFRVOGYO 170
DB 134 KALSELBGLANNVQYLTLAEEMKENPNSRALRDVRNREILDSLFTQYMPSERYTNE 193
QY 171 LLLLEPFOAANMHSFRDVLNADENGISAATLTQYNTLAKNTTBYSNCTNYOTA 230
DB 194 VPELTVYQAAVHLHLLKODASIFGEWGSSTYINNYDRQMKLAEYSDHCCKVWEYG 253
QY 231 FPGIN---TLHDMLEFRTYMFANFEVYSIWSLFKYOSLIVSSGANL---YASGSGP 282
DB 254 LAKLGTSAKQWVDYNOFRSEMTLVLDVVALFPNDRTYRMYETKQLTREYTDPLGA 313
QY 283 QQTQSTQDMPFLXSLFQVNSNYVANGSGARLTOTFPNIGLPGTTTHALLAR--- 339
DB 314 VNVSSIGS--WYDKAPSFVIESSVY-----RPHVFDYITGLVYQSSISASARYR 365
QY 340 -----VNVSGVSSGDIGAVF--NONF--SCSTFLPLLPFRSWLSDSGDRGVNTVT 390
DB 366 HMAHQIISYHRIFSQDNIHKOMYGTQNLHSTF-----DPT 402
QY 391 N---WQTESFESTGLRCGAFTRKNSNTPEDY-FIRNISGV-----LYVRNEDLRRL 441
DB 403 NYDIYKTLKDAVL-----LDIVFPGYTYI--FPGMEVEFEPVWQNLNTRKTL 449
QY 442 HYNELR-----NIESPS-----GTPGGLRAYMVSVH 467
DB 450 KNPVSKDIIAGTRDSLELPETSQPNYBESYHRLCHITSIPAGSTGLGVVPSWTH 509
QY 468 NRKNNTYAVHENG-TMI-----HLAPF-----DYTGT-----ISPHTATVQNNQ 506
DB 510 RSDADLINAVHSDKITQIPVVKVSDLABSITGGPNNTVVSGBPFGGGLIKYIRNGVISH 569
QY 507 TETFLSEFGNQGDSLRFESQNTT-----ARYTL-RGNQNSYNYL 545
DB 570 MRYKISDINKEYSMRIRYASANNTEFYINPSEENVKSHAKTMNRGELTYNNK 623

```

```

RESULT 8
US-10-032-717-4
; Sequence 4, Application US/10032717
; Publication No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flammagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins with
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans

```

FILE REFERENCE: 35718/237005
 CURRENT APPLICATION NUMBER: US/10/032,717
 CURRENT FILING DATE: 2001-10-23
 PRIOR APPLICATION NUMBER: 60/242,838
 PRIOR FILING DATE: 2000-10-24
 NUMBER OF SEQ ID NOS: 48
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 1210
 TYPE: PRT
 ORGANISM: Bacillus thuringiensis
 US-10-032-717-4

Query Match 8.1%; Score 269.5; DB 14; Length 1210;
 Best Local Similarity 22.7%; Pred. No. 2,6e-15;
 Matches 135; Conservative 91; Mismatches 221; Indels 147; Gaps 24;

QY 53 IGVTVSSFL-LKKVSLIGKRLISELMGLIFPSGSNTLMODILRETOPLNORLNTDTLA 111
 DB 76 IYGLSLGLSVFVGVIVS--LYTGLDILIPSGGQSGWEIFMGVVELINOKIAEVARN 133
 QY 112 RVNAELBGLQANIREFNQOVNPL-NFTQNPVLSITSSVNTMOQLFLNRLPOFRYQYQ 170
 DB 134 KALSELBGLGNVQLVLTALBEMKENPVGSRALRDYRNFFELLSFTQYTPSFRTVTFE 193
 QY 171 LLLPLPFAQANMHLSEFIDVVLNADENGLSAATLRTYQNYLKNVTEYSNVCINTYOTA 230
 DB 194 VFLVTVQAANLHLILDASIFBEGWGSTTINNYDRQMKLTAEVSDHCVMWYETG 253
 QY 231 FPGALN---TRLDMLERTYVFLNVEYVSIKSLFKYQSLVSSGANL---YASGGSP 282
 DB 254 LAKLKGTSKQWVDVYQFRRERTLVLDVVALPNNYDTRTYMEKQLFREYVTDPLGA 313
 QY 283 QCTGTSQDMPFLYSLFQVNSNYVLNGFSGAALQTQFPNIGLPGTTTHALLAR--- 339
 DB 314 VAVSSIS--WYDKASIFGVIESSVI-----RPHVFDYITGLVTVQSRSSIRYIR 365
 QY 340 -----VNYSGVSSGDLGAVP--NONF-SCSTFLPPLTTPVMSWLDSSDRGVNVT 390
 DB 366 HWAGHQSISYHIFSDNIKOMYGNONLHSTFT-----DFT 402
 QY 391 N---WQTESFESTLGLRCGAFARQNSNYPDY-FIRNISGV---LVARNEDLRRL 441
 DB 403 NYDIYKTLSDAVL-----LDIVPGLTYI--PFGMPVEYEFVNNQANTRKTL 449
 QY 442 HNEIR-----NIESPS-----GTPGGLRANVVSVH 467
 DB 450 KNPVSKDIIAGTRDSELELPETSDQPNIESYSHRLCHITSIPATSGTGLVPVFSWTH 509
 QY 468 NRKNIVAVHENG-TWI-----HLAPE-----DYTGFT---ISPIHATOVNNO 506
 DB 510 RASADLVNVAHSDKITQIPVVKVSDLAPEITGCFNNTVVSAGPFGCGGILKINGVILSH 569
 QY 507 TETPISSEKFGQSDSLRFSQSTT-----ARYTL-RQNGNSNLYX 545
 DB 570 MKVKISDINKESMRIRYASANNTEFYINPSEENVKSHQKTMNGALTYNKP 623

RESULT 9
 US-09-756-643-2
 Sequence 2, Application US/09756643
 Patent No. US20010026939A1
 GENERAL INFORMATION:
 APPLICANT: Rice, Douglas
 APPLICANT: Carozzi, Nadine
 APPLICANT: Rajasekaran, Kanniah
 APPLICANT: Rangan, Thirumale
 APPLICANT: Yemofsky, Richard
 APPLICANT: Lotstein, Richard
 APPLICANT: De Fiamond, Annick
 TITLE OF INVENTION: Insecticidal Cotton Plant Cells
 FILE REFERENCE: S-16768E

CURRENT APPLICATION NUMBER: US/09/756,643
 CURRENT FILING DATE: 2001-01-08
 PRIOR APPLICATION NUMBER: 08/218,697
 PRIOR FILING DATE: 1994-03-28
 PRIOR APPLICATION NUMBER: 07/759,969
 PRIOR FILING DATE: 1991-09-16
 PRIOR APPLICATION NUMBER: 07/274,452
 PRIOR FILING DATE: 1988-11-18
 PRIOR APPLICATION NUMBER: 07/122,109
 PRIOR FILING DATE: 1987-11-18
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 2
 LENGTH: 1155
 TYPE: PRT
 ORGANISM: Bacillus thuringiensis
 US-09-756-643-2

Query Match 8.1%; Score 268; DB 9; Length 1155;
 Best Local Similarity 22.7%; Pred. No. 3.3e-15;
 Matches 159; Conservative 99; Mismatches 272; Indels 170; Gaps 29;

QY 64 K---VGSIGKRLISELMGLIFPSGSNTLMODILRETOPLNORLNTDTLARVAELB 119
 DB 49 EFPAGAGFVIG--LVDIIMIGRPS---QMDAFVYQIBGLINQRIEERFARNQASRLBEG 102
 QY 120 LQ-----ANIRENQOVNPLNFTQNPVLSITSSVNTMOQLFLNRLPOFRYQYQL 172
 DB 103 LSNLYQVASEPREE-----ADPTNPLREEMRIGFNMSALTLTAIPFAVQNTQV 156
 QY 173 LPLPFAQANMHLSEFIDVVLNADENGLSAATLRTYQNYLKNVTEYSNVCINTYOTAF 232
 DB 157 LLSVYQAANLHLILDASIFBEGWGSTTINNYDRQMKLTAEVSDHCVMWYETG 216
 QY 223 ---GLTRLDML---ERTYVFLNVEYVSIKSLFKYQSLVSSGANLXASGGSPQQT 286
 DB 217 RWGQPSDR--DWIRNQFRRERTLVLDVSLFP-----NYDSKTYPIRTV 260
 QY 287 SFTSODMPFLYSLFQVNSNYVLNGFSGA-----RLTQFPNIGLPGTTT--- 332
 DB 261 SQLR-----EITNPLENFDGSPFGAOGIGSIRSPLMDILNISTITVDAHR 311
 QY 333 -----HALLAARNVSGVSS-----GDIGAVNRQNFSCSTFLPPLTTPVMSWLDSS 381
 DB 312 GEYWSGHQIMASPVGSPGPEFTFLYGTWG---NAAPOQRTVAQJGQVYRTLSSTL 366
 QY 382 DRGCVNTVMQTESFESTLGLRCGAFARQNSNYPDYIR-----NISGVPLVVRNE 435
 DB 367 YRRPFINGINNQ-----QLSVLDGTEFAYGTSNLSAVYRKSQTVSLDEIPQNNV 420
 QY 436 DLK-----RPLAYNIRNIESPSCGGLRANVSVNKR---NNIVAVHE----- 478
 DB 421 PPRQGSRLSHSVSFRSGFSNSV-SIRAPFMSWIRHAEENNTIIPESQTOIPLTKS 479
 QY 479 ---NGTMHLAPEDYGTFTISPIHATOVNNOTRTISEKFGQSDSLRFSQSTTARYT 534
 DB 480 TNGSGSVYKGP---GFT-----GGLLR--RTSPQIST 510
 QY 535 LRGN-----GNSYNLXLRVSSLSNSTIRTYNGRVYTRASNVTNTNNOQVNDARFLDI 589
 DB 511 LRNVITAPLSQRYRIRYASTNTLQFTHSIDGSRINQGSFATMS--GSLNLOGSFRTV 569
 QY 590 NMGNVVASDNTVPLDINV--TFNSGTQFELNMINFEVTNL 628
 DB 570 GFTTFNFSNGSSVFTLSAHVENSNEVYIDRIEVAEV 609

RESULT 10
 US-09-988-462-9

```

; Sequence 9, Application US/09988462
; Publication No. US20030046726A1
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
;         Desai, Nalini M.
;         Lewis, Kelly S.
;         Kramer, Vance C.
;         Warren, Gregory W.
;         Evola, Stephen V.
;         Crossland, Lyle D.
;         Wright, Martha S.
;         Merlin, Ellis J.
;         Launis, Karen L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Syngenta Biotechnology, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/988,462
; FILING DATE: 20-NO. US20030046726A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/547,422
; FILING DATE: 11-APR-2000
; APPLICATION NUMBER: US 08/459,504
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Weigert, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-188051
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1155 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
;
; US-09-988-462-9
;
; Query Match      8.1%; Score 268; DB 11; Length 1155;
; Best Local Similarity 22.7%; Pred. No. 3.3e-15;
; Matches 159; Conservative 99; Mismatches 272; Indels 170; Gaps 29;
;
; QY 6 NNGRTTICDANYVVAHDPSPFEHKS LDTIRKEMWERT--DHSLYVAFIVGVSSFLTK 63
; DB 3 NNPINIECIYPNCLT-----NPEVEVLGERIEIVGYTPIDISL-----SLTOPILS 48
; QY 64 K-----VGLIKRIILSELMLFSPSGSTNLMQDILAEIQPLNRLNTDTTARVNAELRG 119
; DB 49 EYVGAAGVILG--LVITITIGLIGS---QMDAFVQIEQLINQRIEFPARNOQALSRLEG 102
; QY 120 IQ-----ANIEFNOQVDFNLPTONPVPLSITSSVNTVQQLFLNRLFORVQYQL 172
; DB 103 LSNLYOIVASFRFENE-----ADPTNPALREMRIOFNDNMSALTATPILFVQNVQVP 156

```

```

; QY 173 LLEPLAQAAMHLSPIRDVYVNADEMGISAATLRTYQNTLKNYTTERTSYNCINTYTAR 232
; DB 157 LLSVYQANHLHSVLRDVSFQRMGPDATINSKXNDLRLGNVTDARAVENTYGLE 216
; QY 233 ---GLNTRLDHML---EFTYWFILNVEEYISWLSFKYOSLLVSSGANLYASGSGPOQTO 286
; DB 217 RWGCPDSR--DMIRYNQFRRELTIVLDIVSLP-----NDSRTYIRIV 260
; QY 287 SFTSGDWFFLYSLFQVNSNYVANGPSGA-----RLQTPPNIGLPGITTT----- 332
; DB 261 SOLTR-----ELYTPVLENPDSPFGSAQGIIEGINSPLHMDILNLSITTYDAHR 311
; QY 333 -----HALLAARVNSGCVS-----GDGAVFQNSGCSFTPLPLTPFASWIDSQS 381
; DB 312 GRYWSGHQIMASPVFGSGPEFTPLVGTWG-----NAPQORIVAGLGQVVRTLSL 366
; QY 382 DRGVNVTVMQTESPESSTGLRGAFNANPNPDYFIR-----NISGVLVARE 435
; DB 367 YRRPNNIGINN-----QLSVLDGTEFAVGSNSNLSAIVYRKSGTVDLSDELIPQNNV 420
; QY 436 DLR-----PLHYNEIRNIESPSGTPGGLRAYVSVNHRK--NNIYVHE----- 478
; DB 421 PPROGFHRLSHVSMFRSGFSNSV--SIRAPWFMIHRSALFPNNIIPSSQITQIPLTKS 479
; QY 479 -----NGTMIHAPEDYGTFTSPIHATQVNNQTRPTIEKFGNGDGLRPGQNTTART 534
; DB 480 TMLSGTSVYKGP-----GPT-----GGDLR--RTSPGQIST 510
; QY 535 LRGN-----GNSNYLYRVSSLSNSTRVTINGRVTASVNTTNNQVNDGARPLDI 589
; DB 511 LRVITAPLSQRYRVARIRASTTLMQPHSISIDGRPIQNGNSATMS--GSLNQSQSFRTV 569
; QY 590 IMGVVVASDNTVYPLDINV--TFNSGTQFELMNMVPTNL 628
; DB 570 GPTTFPNSGSSVFTLSAHVFNNGMNYIIDLIEVPVAV 609
;
; RESULT 11
; US-09-988-462-11
; Sequence 11, Application US/09988462
; Publication No. US20030046726A1
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
;         Desai, Nalini M.
;         Lewis, Kelly S.
;         Kramer, Vance C.
;         Warren, Gregory W.
;         Evola, Stephen V.
;         Crossland, Lyle D.
;         Wright, Martha S.
;         Merlin, Ellis J.
;         Launis, Karen L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Syngenta Biotechnology, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/988,462
; FILING DATE: 20-NO. US20030046726A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/547,422

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Fri Aug 15 11:51:35 2003

us-10-040-906a-2.rapb

Page 8

FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Weig, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1181 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-988-462-11

Query Match 8.1% Score 268; DB 11; Length 1181;
Best Local Similarity 22.7%; Pred. No. 3.5e-15;
Matches 159; Conservative 99; Mismatches 272; Indels 170; Gaps 29;

6 NNGRTTICDANYVAHDPFSEHKSLDTIRKEMEMKRT--DHSLYVAPVIGTVSSFLK 63
3 NNPNINECIYNCLS-----NPEVEVLGGERITGYTPIIDSL-----SLTQPLLS 48
64 K---VGSILGRKIISELMLIFPSSGSTMMODILRETEQFLNORLNTDTTLARVNAELG 119
49 EFPVGAQFVIG--LVDIIMGIFGPS-----QMDAFVQIEQLNRIEFAFNQAIISRLG 102
120 LQ-----ANIRENQOVNPLNPLONPPLSTISSVNTYQOLFLNRLPORVQVQL 172
103 LSNLYQIVASEFWE-----ADPTNPALEKEMRIQFNDNSALTTAIPFAVNTQVP 156
173 LPLPFAQAMHLSPFRDVLNADENGLSALTATRYQVYLNKYTYTESYNCINTYQVAFR 232
157 LLSYVQANLHLSVIRVSVFGQRKGFDAITNSRNDLRLIGNVTDHAVRWYNGLE 216
233 ---GLNTRLHDL---ERTTMEPLNVEYYSIWSLFXQSILVSSGAMLYAGSGPQQT 286
217 RVMGPDR--DMIRNQRRELTLVLDIVSLFP-----NDSRTPIRIV 260
287 SETSQDWPFLYSLFQVNSNYVANGFSGA-----RLTQTFNIGGLPQTITT----- 332
261 SGLR-----ELYNPVLNFPDGFSGAQIGSIRSPLMDILNSITTYTDMR 311
333 ---HALLARVNYSGVSS---GDIQVFNONSCTFLPPLPLPFRSWLDSGS 381
312 GEYYSGHQIMASPVFSGPEFTPLIYING---NAPQQRIVAQLOGQYVRLSLT 366
382 DRGAVNTVNMQTESFEFTLGRCAFTARQNSNYFPDYFR-----NISGVPLVNE 435
367 YRRPNTGINNQ-----OLSYLDGTFAVGTSSNLSAVYRKSGTVDSIDEIPONNNV 420
436 DLK-----RELHANEIRNIESPGTGGALAAVVSVAHRK---NNIYAVHE----- 478
421 PPRGFSHRLSHVSMRSGFSNSV-SIIRAPFVSHRSALFNKIIIPSSQITQPLRKS 479
479 ---NGTMILAPEDYTGFTTSPHATQVNNQRTFISEKFGQDGLRFEQSNNTARYT 534
480 TVLSGTSVYKGP---GFT-----GGDILR--RTSGQIST 510
535 LRGN-----GNSYNLKLARVSSLSGNTIRVTINGRVYTAANVTITNDGVNDGARFADI 589
511 LKVNITAPLSORIRVIRASTTNLQRTISIDKPLINGNCSNAMS--GSLQSSFTV 569
590 NMGNVASDNTNVPDLIN--TNSGTQELNMTMPTNVL 628

DB 570 GTTFPNSGSSVFTLSAHVNSGNEVYIDRIEFPVPAEV 609

RESULT 12
US-09-988-462-13
Sequence 13, Application US/09988462
Publication No. US20030046726A1
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalin M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crosland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Syngenta Biotechnology, Inc.
STREET: 3054 Cornwalis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-NOV-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Weig, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1181 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-988-462-13
Query Match 8.1% Score 268; DB 11; Length 1181;
Best Local Similarity 22.7%; Pred. No. 3.5e-15;
Matches 159; Conservative 99; Mismatches 272; Indels 170; Gaps 29;

6 NNGRTTICDANYVAHDPFSEHKSLDTIRKEMEMKRT--DHSLYVAPVIGTVSSFLK 63
3 NNPNINECIYNCLS-----NPEVEVLGGERITGYTPIIDSL-----SLTQPLLS 48
64 K---VGSILGRKIISELMLIFPSSGSTMMODILRETEQFLNORLNTDTTLARVNAELG 119
49 EFPVGAQFVIG--LVDIIMGIFGPS-----QMDAFVQIEQLNRIEFAFNQAIISRLG 102

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QY 120 LQ-----ANIRENOQVNFPLNPTONPVLSTTSVNTMOQLFLNRLPOFRVGYOLL 172
DB 103 LSNLYOIVASFRME-----ADPTNPALREKRIQFNPMNSALTPTALPLFAVQNVYV 156
QY 173 LPLPFAQANMHLSTIRDVYLNADDEWISATLRYQNYLKYNTTESNYCINTYQAFR 232
DB 157 LLSVYQAAHLSTLSDVSVFGQRFDAATINSRNDLTRLIGNYTDHVRVWYNGLE 216
QY 233 ---GLNTRLHDML---EFTYMFANFEVYSIWSLFFYQSLVSGANLYASGSGPOQTO 286
DB 217 RWGPDSSR--DWIRNOFRRELTLTVLIVSLFP-----NYDSRYPIRTV 260
QY 287 SFTSDMPFLVSLFOVNSNYVINGPSGA-----RLTQFPNIGLPGTTTT----- 332
DB 261 SOLTR-----EITNVLENFDSFRSQAQIGSIRSPHLMIDLINSITLYDARH 311
QY 333 -----HALLAANVNSGGVSS---GDIGAVFNQFSCSTFLPPLLTTPVNSMLDSSG 381
DB 312 GEYWSGHQIMASPVGSGPEFFPLYGTMG-----NAAPQRIVAQJGQVYRTLSSTL 366
QY 382 DRGVVTVYNNQTSFESTLGRCAFTARNSNYPPDYFIR-----NISGVPLVYRNE 435
DB 367 YRRFPNIGINNQ-----QLSVLDGTERAVGTSSNLSAVYKSGTVDSLDELPQNNVY 420
QY 436 DLK-----RPLATNEIRNIESPSGTPGGLARAYVSVHNR--NNIYAVH----- 478
DB 421 PRQGFSHRLSHVSMFSGFSNSV-SIIRAPMFSWTHRSAPFNIIIPSSQITQILTKS 479
QY 479 ---NGTMIHLAPEDYGFITSPHATQVNNQRTFISKFNQDSLRREGSNTARTY 534
DB 480 TMLSGSTSVKGP-----GFT-----GSDILR--RTSPQIST 510
QY 535 LKGN-----GNSYNLVRVSLGNSITRVINGRVYASNVTTTNDGVNDGARFLDI 589
DB 511 LRVNITAPLSORRYRIRYASTTNLQFTISIDGRPINQGNFATWSS--GSLQSGSFRIV 569
QY 590 NMGNVVASDNTVPLDIN--TENSCTOPELMNIMFVPTL 628
DB 570 GTTTFNFSNGSSVFTLSAHVNSGNEYIYDRLEFPAV 609

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RESULT 13

US-09-988-462-15
 Sequence 15, Application US/09988462
 Publication No. US20030046726A1
 GENERAL INFORMATION:

APPLICANT: Kozel, Michael G.

Desai, Nalini M.

Lewis, Kelly S.

Kramer, Vance C.

Warren, Gregory W.

Evola, Stephen V.

Crossland, Lyle D.

Wright, Martha S.

Meilin, Ellis J.

Launis, Karen L.

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-NO. US20030046726A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Weigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1181 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-988-462-15

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Query Match 8.1%; Score 268; DB 11; Length 1181;
 Best Local Similarity 22.7%; Pred. No. 3.5e-15;
 Matches 159; Conservative 99; Mismatches 272; Indels 170; Gaps 29;

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QY 6 NNGRTTICAVYVVAHDPFSFEKSLDTRKEMWKKRT--DHSLYADIVGTSTVSLTK 63
DB 3 NNPINICPIKCL-----NEVEVLGGRIETGYTPIDSL-----SLQFLLS 48
QY 64 K---VSLIGRIILSELMOIIPSGSTNIMODILRETEQFLNQRINTDTLRLVAELIEG 119
DB 49 EYVAGAFVYG--LVLDIMGIFGFS---QMDAFVYQEQILNQRIEERARNAQASRLRG 102
QY 120 LQ-----ANIRENOQVNFPLNPTONPVLSTTSVNTMOQLFLNRLPOFRVGYOLL 172
DB 103 LSNLYOIVASFRME-----ADPTNPALREKRIQFNPMNSALTPTALPLFAVQNVYV 156
QY 173 LPLPFAQANMHLSTIRDVYLNADDEWISATLRYQNYLKYNTTESNYCINTYQAFR 232
DB 157 LLSVYQAAHLSTLSDVSVFGQRFDAATINSRNDLTRLIGNYTDHVRVWYNGLE 216
QY 233 ---GLNTRLHDML---EFTYMFANFEVYSIWSLFFYQSLVSGANLYASGSGPOQTO 286
DB 217 RWGPDSSR--DWIRNOFRRELTLTVLIVSLFP-----NYDSRYPIRTV 260
QY 287 SFTSDMPFLVSLFOVNSNYVINGPSGA-----RLTQFPNIGLPGTTTT----- 332
DB 261 SOLTR-----EITNVLENFDSFRSQAQIGSIRSPHLMIDLINSITLYDARH 311
QY 333 -----HALLAANVNSGGVSS---GDIGAVFNQFSCSTFLPPLLTTPVNSMLDSSG 381
DB 312 GEYWSGHQIMASPVGSGPEFFPLYGTMG-----NAAPQRIVAQJGQVYRTLSSTL 366
QY 382 DRGVVTVYNNQTSFESTLGRCAFTARNSNYPPDYFIR-----NISGVPLVYRNE 435
DB 367 YRRFPNIGINNQ-----QLSVLDGTERAVGTSSNLSAVYKSGTVDSLDELPQNNVY 420
QY 436 DLK-----RPLATNEIRNIESPSGTPGGLARAYVSVHNR--NNIYAVH----- 478
DB 421 PRQGFSHRLSHVSMFSGFSNSV-SIIRAPMFSWTHRSAPFNIIIPSSQITQILTKS 479
QY 479 ---NGTMIHLAPEDYGFITSPHATQVNNQRTFISKFNQDSLRREGSNTARTY 534
DB 480 TMLSGSTSVKGP-----GFT-----GSDILR--RTSPQIST 510
QY 535 LKGN-----GNSYNLVRVSLGNSITRVINGRVYASNVTTTNDGVNDGARFLDI 589

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-NO. US20030046726A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Weigse, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ. ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1181 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-988-462-28

Query Match 8.1%; Score 268; DB 11; Length 1181;
Best Local Similarity 22.7%; Pred. No. 3,5e-15;
Matches 159; Conservative 99; Mismatches 272; Indels 170; Gaps 29;
QY 6 NNGRTTICDANVVAHDPPSEHKSIDTIRKEMWERT--DHSLYVAPIGVTSFILK 63
DB 3 NNPINIECIPYNCIS-----NPEVVLGERIEGTTPIDISL-----SLQFILS 48
QY 64 K---VSLIGKRIISLMLGLIPSGSTNLMODILETEPOFLNQLNTDTLARVNAELG 119
DB 49 EFPVGAQFVLG--LVDIIMGIFPS---OMDAFLVQIEOLINQRIEFPARQAISRLG 102
QY 120 IQ-----ANIEEFNQVDNFINPTONPVPLSITSSVNTMQQLFLNRLPQPRVQYQL 172
DB 103 LSNLYQIYASPREME-----ADPTNPALREEMRIQFNDMSALTTAIPFAVQNYVP 156
QY 173 LLEPFAQAAHMLSPTRDVANLADKGIASATLRTYONYLKNYTESNYCINTYQTAFR 232
DB 157 LLASYVQAANLHLSVLRDVSFGQRMGFDAITINSRYNDLTRLIGNYTDHARVNTGLE 216
QY 233 ---GLNTRLIDML---EFFTYMFLNFEVYSIMSLFKQSLVSSGANLYASGSGPOQTQ 286
DB 217 RVMPDPSR--DWIRYNQFRRLTLTVLDIVSLP-----NYDSRTYPIRTV 260
QY 287 SFTSQDMPLFLFQVNSNYVLNFGSGA-----RLTQTFPIGALPGTTT----- 332
DB 261 SQLTR-----ETYNPVLNPFDSFRSGAQIGSIRSPHMDIINSITTYTDAHR 311
QY 333 -----HALLAARVNSGVSS---GDIGAVFNQNFSCSTFLPPLTFPFRSMLDGS 381
DB 312 GEYYSQHQIMASPVGFSGPEFTFPLYGTWG-----NAAPQQRIVAQGGQYRTLSSTL 366
QY 382 DRGGVNTVNMQTESFESTLGLRGAFTARGNSNFPDYFR-----NISGVPLVVRNE 435
DB 367 YRRFENIGINNQ-----QLSVLDGTEFAVGTSSMLPSAVYRKSGTVDLDEIPQNNV 420
QY 436 DLR-----RPLHYNIEIRNIESPGTGLRAYMVSVHNK---NNIYAVHR----- 478
DB 421 PPGQGFHRLSHVSMFRSGFSNSSV--SIRAPMFSWIRSAEFNNIIPESQITQIPLTGS 479

QY 479 -----NGTMHAPEDYTGFTSPIHATQVNNQTRTFISKEGNOGDSLRPEOSNTTART 534
DB 480 TNLGSGISVVKGP---GFT-----GGDILR--RTSPQIST 510
QY 535 LRGN-----GNSYNYLRYVSLGNSITRTVINGRVYVYASNVNTTNNNDGVNDGARPLDI 589
DB 511 LRNVITAPLSQRYRVARIRYASTTTLQPHISIDSRPIINGNFSATMS--GSLQSGSFRTV 569
QY 590 MNGNVASDNTNVPDIDIN--TPNSGTQFELAMIMFVPTNL 628
DB 570 GTTTPNFNSGSSVFTLSAHVFNSGNEVYIDRIEFPVPAEV 609

Search completed: August 14, 2003, 18:14:02
Job time : 37 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 14, 2003, 18:09:22 ; Search time 27 seconds
(without alignments)
2251.060 Million cell updates/sec

Title: US-10-040-906a-2

Perfect score: 3314

Sequence: 1 MNVYVNGRTTICDANVVA.....CTQELMIMVPIVNLPIY 632

Scoring table: BLOSUM62

Gapop 10.0, Gapept 0.5

Searched: 283308 seqs, 9616882 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: PIR76:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3048.5	92.0	633	2	C32053 paraaporal crystal
2	3010.5	90.8	633	2	D32053 paraaporal crystal
3	2545	76.8	622	2	S17402 paraaporal crystal
4	336.5	10.2	643	2	A43647 paraaporal crystal
5	327.5	9.9	719	2	I39815 insecticidal prote
6	324.5	9.8	719	2	S25383 paraaporal crystal
7	324.5	9.8	719	2	I39815 insecticidal prote
8	310.5	9.4	719	2	I40590 paraaporal crystal
9	307	9.3	1157	1	S49247 paraaporal crystal
10	294.5	8.9	1176	2	A48970 paraaporal crystal
11	282.5	8.5	1176	2	UT0241 paraaporal crystal
12	280.5	8.5	934	2	A23798 paraaporal crystal
13	277.5	8.4	380	2	B43459 paraaporal crystal
14	277	8.4	1181	2	A41052 paraaporal crystal
15	276.5	8.3	1176	2	UC2219 paraaporal crystal
16	275.5	8.3	1228	2	S00873 paraaporal crystal
17	273	8.2	1155	2	A26513 paraaporal crystal
18	271.5	8.2	1176	2	A22617 paraaporal crystal
19	271.5	8.2	1176	2	S02215 paraaporal crystal
20	269	8.1	1155	2	S02134 paraaporal crystal
21	268	8.1	1155	2	UD0002 paraaporal crystal
22	268	8.1	1156	2	A29125 paraaporal crystal
23	267.5	8.1	1178	1	US83X paraaporal crystal
24	267	8.1	1155	2	I39838 paraaporal crystal
25	265	8.0	1174	2	A42459 paraaporal crystal
26	264.5	8.0	1160	2	I40589 paraaporal crystal
27	264	8.0	1174	2	S33649 paraaporal crystal
28	262.5	7.9	1156	2	A29838 paraaporal crystal
29	261.5	7.9	1172	2	S33689 paraaporal crystal

30	259	7.8	1155	2	S11446 paraaporal crystal
31	259	7.8	1177	2	A43785 paraaporal crystal
32	255.5	7.7	649	1	UH0261 paraaporal crystal
33	253	7.6	618	2	S11445 paraaporal crystal
34	253	7.6	1138	2	A48944 paraaporal crystal
35	250	7.5	652	2	A27323 paraaporal crystal
36	249.5	7.5	652	2	I39811 paraaporal crystal
37	247.5	7.5	659	2	S10228 paraaporal crystal
38	244	7.4	1160	2	S32647 paraaporal crystal
39	237	7.2	613	2	UC6033 paraaporal crystal
40	230.5	7.0	685	2	UC7140 paraaporal crystal
41	229.5	6.9	1189	2	S00944 paraaporal crystal
42	225	6.8	823	2	S04181 paraaporal crystal
43	218.5	6.6	1171	2	A37829 paraaporal crystal
44	218.5	6.6	1171	2	I40572 paraaporal crystal
45	216	6.5	1154	2	S39536 paraaporal crystal

ALIGNMENTS

RESULT 1

C32053

paraaporal crystal protein BI - Bacillus thuringiensis subsp. kurstaki

N:Alternate names: paraaporal crystal protein P2

C:Species: Bacillus thuringiensis subsp. kurstaki

C>Date: 13-Jul-1989 #sequence_revision 13-Jul-1989 #text_change 15-Oct-1999

C:Accession: C32053; A29913

R:Widmer, W.R.; Whiteley, H.R.

J. Bacteriol. 171, 965-974, 1989

A>Title: Two highly related insecticidal crystal proteins of Bacillus thuringiensis subsp. kurstaki

A:Reference number: A32053; WUID:89123178; PMID:2914879

A:Accession: C32053

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1633 <WID>

R:Donovan, W.P.; Dankocskik, C.C.; Gilbert, M.P.; Gawron-Burke, M.C.; Groat, R.G.; Carlb

J. Biol. Chem. 263, 561-567, 1988

A>Title: Amino acid sequence and entomocidal activity of the P2 crystal protein. An ins

A:Reference number: A29913; WUID:88087146; PMID:3121615

A:Accession: A29913

A:Molecule type: DNA

A:Residues: 1587, 'FRY' <DON>

C:Genetics:

A:Gene: cryBI

Query Match 92.0%; Score 3048.5; DB 2; Length 633;

Best Local Similarity 90.7%; Pred. No. 6.7e-200;

Matches 574; Conservative 34; Mismatches 24; Indels 1; Gaps 1;

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DB	1	MNVYVNGRTTICDANVVAHDPSPFHKSLDTIKEMEMKRTDHSYVAIVGTVSSSF	60
QY	61	LLKTVGSLIGKRIILSELWGILFPGSGTNMODILRETFOLNORLWDTLAVNAELGL	120
DB	61	LLKTVGSLIGKRIILSELWGILFPGSGTNMODILRETFOLNORLWDTLAVNAELGL	120
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QY	181	ANMHLSTIRDVVIANDEWGISAAITRTYQNYLKNYTESNYCINTYQAFRGLNTRLHD	240
DB	181	ANMHLSTIRDVVIANDEWGISAAITRTYQNYLKNYTESNYCINTYQAFRGLNTRLHD	240
QY	241	MLEFRITMPEANFEVYSIWSLFKQSLVSGANLVYSGSGPOQOSFISODMPETLSLF	300
DB	241	MLEFRITMPEANFEVYSIWSLFKQSLVSGANLVYSGSGPOQOSFISODMPETLSLF	300
QY	301	QVNSNYLVAGSGARLTOTPNIGLPGTTTHALLARVNSGVSSGDIQAV-FNQN	359
DB	301	QVNSNYLVAGSGARLTOTPNIGLPGTTTHALLARVNSGVSSGDIQAV-FNQN	359
QY	360	QVNSNYLVAGSGARLTOTPNIGLPGTTTHALLARVNSGVSSGDIQAV-FNQN	360
DB	360	QVNSNYLVAGSGARLTOTPNIGLPGTTTHALLARVNSGVSSGDIQAV-FNQN	360

Qy	360	SGSTLEPLLEPLPPFRASMLDSGSDRGVATVYNNQTSFSTLGLHCOAFTRKNGSNVFPD	419
Qy	361	NCSTVLPPLSPFRFVASMLDSGTRGCVATSNMQTESPOTTLISRCQAFSARNGSNVFPD	420
Db	361	NCSTVLPPLSPFRFVASMLDSGTRGCVATSNMQTESPOTTLISRCQAFSARNGSNVFPD	420
Qy	420	YVIRNISGVPLVYVANDLRPLHAYEININISPEGTFGCGIARAYMSVYANRNINIVAHEN	479
Qy	421	YVIRNISGVPLVYVANDLRPLHAYEININISPEGTFGCGIARAYMSVYANRNINIVAHEN	480
Db	421	YVIRNISGVPLVYVANDLRPLHAYEININISPEGTFGCGIARAYMSVYANRNINIVAHEN	480
Qy	480	GMTHLAEDYTGCTLSPIHATOVNNORFTISKPEKNQODSLRFEQSNNTAARTLLRGNG	539
Qy	481	GMTHLAEDYTGCTLSPIHATOVNNORFTISKPEKNQODSLRFEQSNNTAARTLLRGNG	540
Db	481	GMTHLAEDYTGCTLSPIHATOVNNORFTISKPEKNQODSLRFEQSNNTAARTLLRGNG	540
Qy	540	NSRYNKLKLVSSLGKSTRTATNGRYVTSANNNTTNNDDGNNNGARPLDIMMGVVAASN	599
Qy	541	NSRYNKLKLVSSLGKSTRTATNGRYVTSANNNTTNNDDGNNNGARPLDIMMGVVAASN	600
Db	541	NSRYNKLKLVSSLGKSTRTATNGRYVTSANNNTTNNDDGNNNGARPLDIMMGVVAASN	600
Qy	600	TVNPLDINVTNNGCTOPELNNIMFVPTNLPITY	632
Qy	601	TVNPLDINVTNNGCTOPELNNIMFVPTNLPITY	633
Db	601	TVNPLDINVTNNGCTOPELNNIMFVPTNLPITY	633

RESULT 2

D32053
paraporal crystal protein B2 - *Bacillus thuringiensis* subsp. *kurstaki*
CSpecies: *Bacillus thuringiensis* subsp. *kurstaki*
CDate: 13-Jul-1989 #sequence_rev13-Jul-1989 #text_change 15-Oct-1999
CAccession: D32053; S12396
R:Widner, W.R.; Whiteley, H.R.
J. Bacteriol. 171, 965-974, 1989
A>Title: Two highly related insecticidal crystal proteins of *Bacillus thuringiensis* subsp. *kurstaki*
A.Reference number: A32053; MUID:89123178; PMID:2914879
A.Accession: D32053
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-633 <MID>
R:Dankocsi, C.; Donovan, W.P.; Jany, C.S.
Mol. Microbiol. 4, 2087-2094, 1990
A>Title: Activation of a crystal protein gene of *Bacillus thuringiensis* subsp. *kurstaki*
A.Reference number: S12396; MUID:91211618; PMID:2089222
A.Accession: S12396
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-633 <MID>
A.Cross-references: EMBL:X55416; NID:g40311; PIDN:CAA93075.1; PID:g40312

[illegible]

Qy	360	SCSEFPEPLLPFVRSALDGSRCGVATVYNNQTSFESTLGLRCALFARQNSNYPD	4.19
Qy	361	NCSEFPEPLLPFVRSALDGSRCGVATVYNNQTSFESTLGLRCALFARQNSNYPD	4.20
Db	361	NCSEFPEPLLPFVRSALDGSRCGVATVYNNQTSFESTLGLRCALFARQNSNYPD	4.20
Qy	420	YFTRNLSGPELVNEDLRPEHYNEINIESPSGPGCLRAYVVSVHNNKNNIYAVHN	4.79
Db	421	YFTRNLSGPELVNEDLRPEHYNEINIASPSGPGCLRAYVVSVHNNKNNIYAVHN	4.80
Qy	480	GTMIHLAPEDYGFETSPHATVNNQRRPISSEKNGGDSLFPEOSNTAYTLRANG	5.39
Qy	481	GSMLHAPEDYGFETSPHATVNNQRRPISSEKNGGDSLFPEOSNTAYTLRANG	5.40
Db	481	GSMLHAPEDYGFETSPHATVNNQRRPISSEKNGGDSLFPEOSNTAYTLRANG	5.40
Qy	540	NSNYKLARSISGNSLTRYNINGRYTTASNNVTYNNDDVNNNGARFLDINNQNVASDN	5.99
Qy	541	NSNYKLARSISGNSLTRYNINGRYTTATVNTTYNNDDVNNNGARFSDINIGNVASSN	6.00
Db	541	NSNYKLARSISGNSLTRYNINGRYTTATVNTTYNNDDVNNNGARFSDINIGNVASSN	6.00
Qy	600	TNPPLDINTNTRSGIOPELNNIMFVPTLAPPLY	6.32
Qy	601	SDVEPLDINTNLVLSGIDPLNNILNLPVNIISLPL	6.33
Db	601	SDVEPLDINTNLVLSGIDPLNNILNLPVNIISLPL	6.33

RESULT 3

S17402
 parasporeal crystal protein cry2aet - *Bacillus thuringiensis* plasmid
 N.Alternate names: delta-endotoxin; parasporeal crystal protein cryIIc
 C.Species: *Bacillus thuringiensis*
 C.Date: 22-Nov-1993 #sequence_rev1510 10-Nov-1995 #text_change 01-Dec-2000
 C.Accession: S17402
 R.Wu, D.; Cao, X.L.; Bai, Y.Y.; Aronson, A.I.
 FEBS Microbiol. Lett. 81, 31-36, 1991
 A.Title: Sequence of an operon containing a novel delta-endotoxin gene from *Bacillus thuringiensis*
 A.Reference number: S17400
 A.Accession: S17402
 A.Status: preliminary
 A.Molecule type: DNA
 A.Residues: 1-622 <WU>
 A.Cross-references: EMBL:X57252; NID:g40283; PIDD:CMA40536.1; PID:g40286
 C.Genetics:
 A Genome: plasmid
 C.Keywords: delta-endotoxin

Query Match	76.8%	Score 2545	DB 2	Length 622
Best Local Similarity	78.9%	Pred. No. 1,3e-165		
Matches	501	Conservative 45	Mismatches 73	Indels 16
				Gaps 8
Qy	1	MMNNVANNGRRTTICDAAYNNVVAADPFSEFHSJDTITREKMEKRTDHSLYAVATIGVYSSF	60	
Db	1	MMVTVANNGRNTTCAHANNVVAADPFSEFHSKSLNTEKMEKMRDHSLYAVATIGVYSSF	60	
Qy	61	LLKRVGSLGKRIILSELMGILFPGSGSTLMODLTRETFQFNNKNTLNDTLAAVNALEGL	120	
Db	61	LLKRVGSLGKRIILSELQNLIFPGSGSIDLMQELIRATEQFINGNLNDTLGRVNALEGL	120	
Qy	121	QANIRENQOQVNFNFANPONPVPPLSTTSVNTVMQOLFNLRLPQFVQGIQLLLPLFPOA	180	
Db	121	QANVAEENRQVNFNFANPONPVPPLAIDSVNTLQOLFSLRLPQFQIYQYQLLLPLFPOA	180	
Qy	181	ANNHLSITDVTYLANDDEMGISAALTITQONTLKNYTTESNVCNTYQAPFGLNTRLRHD	240	
Db	181	ANFNLSITRQVTLINDEMGISAALTITRDLKRFHSDSNVCNLPQIRFGLNHLRPD	240	
Qy	241	MLEPFTYVPLNVEYVYSWLSFLKYQGLVYSSGANTYASGSGFOOTSGTSDMPFLYSLF	300	
Db	241	MLEPFTYVPLNVEYVYSWLSFLKYQGLVYSSGANLYASGSG--TGFTRKQMPFLYSLF	298	
Qy	301	QVNSVNYVINGFSGANLYOTFPNTIGSLP-GITTTTHLLAARNYSGVSGSGDIG-AVFNQ	357	
Db	299	QVNSVNYVINGSGARTTTFPNTIGSLPYVHNSLH--PARINTRGVGVSRRSGQANLNQ	355	
Qy	358	NNSGCTELPPLLPVRSKMDSGDGGNNYVVMQTESFEFSTIGLRCGFTARGNSYF	417	
Db	356	NNISITLPLNDLPPIKSLMDSGDDESVASTIMQSGAFETTL-LAFSIFSRAGNSNF	414	

QY 418 PDYPIENISGVLEVRNEDLRRLPHAYNEIRNIESPGTGLRLAYVSVHNKRKNYAYH 477
 DB 415 PDYPIENISGVLEVRNEDLRRLPHAYNEIRNIESPGTGLRLAYVSVHNKRKNYAYH 468
 QY 478 ENGMTLHAPEDYGTFTSPHATONNOTRTTISEKFGQGSGLRFGOSNTATYATLNG 537
 DB 469 ENGMTLHAPEDYGTFTSPHATONNOTRTTISEKFGQGSGLRFGOSNTATYATLNG 528
 QY 538 NENSYNYLYRVSSLSGNTITRTINGRVYASVNTTNNNDGVNDGARFLDINNGVNVAS 597
 DB 529 NENSYNYLYRVSSLSGNTITRTINGRVYASVNTTNNNDGVNDGARFLDINNGVNVAS 587
 QY 598 DNTNVPDLINTFNSGTQFELNIMVPTNLPY 632
 DB 588 ANTNVPLDIQTFNNGNQPFLNIMVPTNLPY 622

RESULT 4

A43647
 paraoral crystal protein cry11aA1 - *Bacillus thuringiensis* subsp. *israelensis*
 C:Species: *Bacillus thuringiensis* subsp. *israelensis*
 C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 01-Dec-2000
 C:Accession: A43647; #sequence_revision 03-Mar-1993 #text_change 01-Dec-2000
 R:Donovan, W.P.; Danko, C.; Gilbert, M.P.
 J:Biotechnol. 170, 4732-4738, 1988
 A:Title: Molecular characterization of a gene encoding a 72-kilodalton mosquito-toxic crystal protein from *Bacillus thuringiensis* subsp. *israelensis*
 A:Reference number: A43647; PMID:89008093; PMID:2902069
 A:Accession: A43647
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-643 <DON>
 A:Cross-references: GB:M31737; NID:9142762; PIDN:AAA22352.1; PID:9142763
 J:Adams, L.P.; Vaisick, J.E.; Whiteley, H.R.
 J:Biotechnol. 171, 521-530, 1989
 A:Title: A 20-kilodalton protein is required for efficient production of the *Bacillus thuringiensis* serotype *delta endotoxin*
 A:Reference number: A32256; PMID:89123065; PMID:2644205
 A:Accession: A32256
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 566-643 <ADU>
 A:Cross-references: EMBL:M22860; NID:9143223; PIDN:AAA22611.1; PID:9143224
 C:Genetics: cryD
 A:Gene: cryD

Query Match 10.2%; Score 336.5; DB 2; Length 643;
 Best local similarity 23.1%; Pred. No. 4,5e-15;
 Matches 167; Conservative 98; Mismatches 257; Indels 201; Gaps 34;

QY 27 EHKSLDTIRKEMEMKRTDHSLY-----VAP---IVGTVSSFLKKGSLIGKRIISE 76
 DB 2 EHKSLDTIRKEMEMKRTDHSLY-----VAP---IVGTVSSFLKKGSLIGKRIISE 76
 QY 77 LMGILPFGSGSTNLMQDILRETEOFNORLNTDLARVAELGQANIREFNQVDNLT 135
 DB 58 VLSILPFGSQPATMEKVRTEVETLLINQKLSQDVNINANERG---IIEVSVDAYIK 113
 QY 136 NPQNPVPLSITSSVVTMOQLFN-----RIPQVRQVQQLLLPLPQANMHSFI 188
 DB 114 QPGFTPA-----TAKGFLNLSGAILIQRLEPQVQYEGVSIALPFOCTHLLTL 164
 QY 189 RDVVLNADWEGISAATLRTYONVYKNTTEYSNYCINTYQAF--RGLNRLDMLPEPTY 247
 DB 165 KDGIAGSAGWFOADVDSFIKLFNOKVLDYRTRLMRYTEBERLCKSLDGLTFPNNM 224
 QY 248 MFLNVEFYVSIKSLFYQSLVSSGAGLVSSGPGQOSTSDWPEFLYSLPQVNSR-- 305
 DB 225 CNLVYPPFPAMSLMKREGLKQSSLSL-----MDYGVSIPIPNVYEW 267
 QY 306 -----YVNGFSGARLQTFPNIGLPGITTTTHALLAARVNSG-----GVSSGDIQAVF 355
 DB 268 GGLVYKLLMGVNOBLTIVKENV-----SFTNEPADIPAREINRGVHPHYDPSGLTWIG 323

QY 356 N---QNFSCSTFLPPLITFVNSMLDSGDRGNTVTNQ----- 393
 DB 324 NGRNTNENFAD-----NNGNEMEVRTQYQPNNEIARDDIINOILTA 369
 QY 394 -----TESFSTLY-----GLRCGAPARSN-----SNY---PPDYPIRNI 425
 DB 370 PAPADLPFKNADINVKFTQWPGSTLYGKNIKQGTQVLSRSRGITIPNYLAVGYITRI 429
 QY 426 SGVPLVYR---NEDLARRPHAYNEIRNIESPG-----TEGRLRAYSVHNKRKNYAY 475
 DB 430 SACRPGVSLANEDL--TTLITNRI--EYDSPTENIIVGAPDNKDP---YKKS--- 479
 QY 476 VHENGTMIHAPEDYGTFTSPHATONNOTRTTISEKFGQGSGLRFGOSNTATYATLNG 532
 DB 480 -----HYLSEPTNDSYVIALQFAEVS--RSFLEDIPPOANDGSIKARFTISNEAK 529
 QY 533 YTLRGNGSYNYLYRVSSLSGNTITRTINGRVYASVNTTNNNDGVNDGARFLDINNG 592
 DB 530 YSIRLN--TGNVTRTKYI---IRVVPYRL--PAGIRVQSSQNGNN---RMLGSFTPA 578
 QY 593 NV-----VASDNTNVPDLINTV--TFNSGTQFELNIMVPTNLPY 632
 DB 579 NANEVWDVETDAPPTENDIGITTSITVALFSSISDSGINSGEWYLSQLFLYKESAFPTQI 638
 QY 629 PPI 631
 DB 639 NPL 641

RESULT 5

139815
 insecticidal protein cryV - *Bacillus thuringiensis*
 C:Species: *Bacillus thuringiensis*
 C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 26-Aug-1999
 C:Accession: 139815
 R:Glenn, A.P.; Williams, R.; Hedges, R.J.
 J:Appl. Environ. Microbiol. 59, 1683-1687, 1993
 A:Title: Screening by polymerase chain reaction of *Bacillus thuringiensis* serotypes for *leucine* subsp. *kurstaki*.
 A:Reference number: 139815; PMID:93298009; PMID:8517758
 A:Accession: 139815
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-719 <PES>
 A:Cross-references: GB:M98544; NID:9142767; PIDN:AAA22354.1; PID:9142768
 C:Genetics: cryV
 A:Gene: cryV
 C:Superfamily: paraoral crystal protein

Query Match 9.9%; Score 327.5; DB 2; Length 719;
 Best local similarity 22.8%; Pred. No. 2,2e-14;
 Matches 162; Conservative 103; Mismatches 271; Indels 173; Gaps 32;

QY 21 HDPSTFEH---SLDTIRKEM--MEWKRTD-----SLY--VAP----- 52
 DB 9 HDSFSSNAKVDKISTDSIKNETDIELOININHDCKKSEVENEPVSASTQGTGIGIAG 68
 QY 53 -IVGTVSSFLKKGSLIGKRIISELMGLIPFGSGSTNLMQDILRETEOFNORLNTDTLA 111
 DB 69 KILGTIGVPAQVAVSLY--SFLIGELM-----PKGR--NOMIEIHEVYELINQKISTYARN 122
 QY 112 RVNAELEGQANIREFNQVDNLFNPTQNPVLSIT--SSVNTMOQLFNRLPQVRVQGYO 170
 DB 123 KALTDKLGGLDLAVYHDSLESVWGRRNTRARSVVVSQYIALELMFOVKLPSPAVSGEE 182
 QY 171 LLLPLPQANMHSFIRDVVLNADWEGISAATLRTYONVYKNTTEYSNYCINTYQAF 230
 DB 183 VPLPPIYQAQNLHLILLRDAISIFKEMGSSSISFTNRYQVBAAGYSIHCYKWTSTG 242
 QY 231 FREL--WTRIRHML---EFTYMLAVFYVSIKSLFYQSLVSSGAGLVSSGAGLVSSGAG 282
 DB 243 LNNLRGTNAESVNRVNOFRDMDTLNVLVLPSPYDQVYPIKTTAOLTRFVYVTAIGT 302

```

OY 283 OQTO-SFTSODM-----PFL-----YSLFOVNSN-YVLNGESG 313
DB 303 VHPHSFTSTWYNNANAPSAIEAAVVRNPHLDLEQVITYSLSRMSNTQYMMWG 362
OY 314 ARLTQFPNIGLPGTTTHALLAARVNSGVSSGDIQAVNQNFSCTFLPPLTPPV 373
DB 363 HXL-EFRTIGGTLNIST-----QGSTVNSINPVLTPFT 394
OY 374 RSMWDSGSDRGVNTVT-----NMQ--TESFESTGLRCGAFTRAGNSNYPD 419
DB 395 SRDYRTRESLAGNMLFLTPQVNGVRVDHFHKFVTHPIAS-----DNFVYFG 441
OY 420 YFRINISGVPLVRNEDLRRLPHVNEIRNIESPSGTPGGLAAVVSVHRKNKIYA-VHE 478
DB 442 Y-----AGTGTQLODSENELEPPAATGQPVYSYHRLSHG-LISASHVKAIVSWTHR 494
OY 479 NGTMHLAPEDYTGFTISPIHATQV-----NNQTRFISEKFG-NQGSILPEQSNTTA 531
DB 495 SA-----DRTN-TIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGDLR--RTNVTG 543
OY 532 RYTLRGNNGN-----SYNLYRVSSLGNSITRTVINGRVYASVNTTNNQVNDNGARF 586
DB 544 RGDIVNINPFAQRVRIRIRASTTDLOPHHSINGKALINQANFSATMR-----GED 596
OY 587 LDINMGAVVASDNTNVPDLINVT-----FNSGTQFELNIMFVPTNL 628
DB 597 LDYKTFRTVGTTPPSFLDQSTFTIGAMNFSNGNEVYIDRIEFVPEV 645

```

RESULT 6

paraaporal crystal protein cryIal - *Bacillus thuringiensis*
 N/Alternate names: delta-endotoxin, paraaporal crystal protein cryV
 C/Species: *Bacillus thuringiensis*
 C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 01-Dec-2000
 C/Accession: S25383
 R/Author: R.; Tipsett, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.
 Moll. Microbiol. 6, 1211-1217, 1992
 A>Title: Identification and characterization of a novel *Bacillus thuringiensis* delta-end
 A/Reference number: S25383; MUID:92265082; PMID:1588820
 A/Accession: S25383
 A/Molecule type: DNA
 A/Residues: 1-719 <TAL>
 A/Cross-references: EMBL:X62821; NID:g40289; PIDD:CAA44633.1; PID:g40290
 C/Genetics:
 A/Gene: cryV
 C/Superfamily: paraaporal crystal protein
 C/Keywords: delta-endotoxin

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Query Match          9.8%; Score 324.5; DB 2; Length 719;
Best Local Similarity 22.8%; Pred. No. 3,5e-14;
Matches 162; Conservative 102; Mismatches 272; Indels 173; Gaps 32;

OY 21 HDPSFEHK-----SLDTRIKEM-MEMKRTDH-----SLY--VAP-----52
DB 9 HOSFSSNAKVDKISTDSIKNETDIELQNIHNECDLCKMSEYENVEPVASITQTCIGIAG 68
OY 53 -IVGTSSFLKKVGSILGKRIISLWGLFPFSGSTNIMODILRETOFANRLNTDTLA 111
DB 69 KILGLGVPPAGVAVSLY-SFLIGELM-----PKGK-NQMEIFMEHVEIINQKISTARN 122
OY 112 RVNAELGLOANIREFNOQVDFNPNTQNPVLSTT-SSVNTMOQLFLNRLPOFRVQYQ 170
DB 123 KALTDKLGIDALAVVHDSLESVWGNRRNTARASVQYALIELMFVQGLDSFVASEE 182
OY 171 LLLLPLFAQANMHSIFRDVVLNADENGISAATLRTQYQYKNTTYSVNCINTYOTA 230
DB 183 VPLPIYAQANLHLLILDASIFGKEWGLSSSEISTFYRQVBERADYSYHCVKWTSG 242
OY 231 FRGL-NTRLHDMU---EFFTYMFLNVEFVYSIMSLFKYQSLVSSGANL---YASGSGP 282
DB 243 LNNLRGTMASVWVRNQFRDMDTLNVLVDLVALPSPYDTQWPIKTTAQLTREYVTDALGT 302

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OY 283 OQTO-SFTSODM-----PFL-----YSLFOVNSN-YVLNGESG 313
DB 303 VHPHSFTSTWYNNANAPSAIEAAVVRNPHLDLEQVITYSLSRMSNTQYMMWG 362
OY 314 ARLTQFPNIGLPGTTTHALLAARVNSGVSSGDIQAVNQNFSCTFLPPLTPPV 373
DB 363 HXL-EFRTIGGTLNIST-----QGSTVNSINPVLTPFT 394
OY 374 RSMWDSGSDRGVNTVT-----NMQ--TESFESTGLRCGAFTRAGNSNYPD 419
DB 395 SRDYRTRESLAGNMLFLTPQVNGVRVDHFHKFVTHPIAS-----DNFVYFG 441
OY 420 YFRINISGVPLVRNEDLRRLPHVNEIRNIESPSGTPGGLAAVVSVHRKNKIYA-VHE 478
DB 442 Y-----AGTGTQLODSENELEPPAATGQPVYSYHRLSHG-LISASHVKAIVSWTHR 494
OY 479 NGTMHLAPEDYTGFTISPIHATQV-----NNQTRFISEKFG-NQGSILPEQSNTTA 531
DB 495 SA-----DRTN-TIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGDLR--RTNVTG 543
OY 532 RYTLRGNNGN-----SYNLYRVSSLGNSITRTVINGRVYASVNTTNNQVNDNGARF 586
DB 544 RGDIVNINPFAQRVRIRIRASTTDLOPHHSINGKALINQANFSATMR-----GED 596
OY 587 LDINMGAVVASDNTNVPDLINVT-----FNSGTQFELNIMFVPTNL 628
DB 597 LDYKTFRTVGTTPPSFLDQSTFTIGAMNFSNGNEVYIDRIEFVPEV 645

```

RESULT 7

insecticidal protein cryVI - *Bacillus thuringiensis*
 C/Species: *Bacillus thuringiensis*
 C/Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 26-Aug-1999
 C/Accession: I39814
 R/Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.
 Appl. Environ. Microbiol. 61, 2402-2407, 1995
 A>Title: Distribution of cryV-type insecticidal protein genes in *Bacillus thuringiensis*
 A/Reference number: I39814; MUID:95314293; PMID:7793960
 A/Accession: I39814
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-719 <RES>
 A/Cross-references: GB:I6338; NID:g540281; PIDD:AAC36999.1; PID:g540282
 C/Genetics:
 A/Gene: cryVI
 C/Superfamily: paraaporal crystal protein

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Query Match          9.8%; Score 324.5; DB 2; Length 719;
Best Local Similarity 22.8%; Pred. No. 3,5e-14;
Matches 162; Conservative 102; Mismatches 272; Indels 173; Gaps 32;

OY 21 HDPSFEHK-----SLDTRIKEM-MEMKRTDH-----SLY--VAP-----52
DB 9 HOSFSSNAKVDKISTDSIKNETDIELQNIHNECDLCKMSEYENVEPVASITQTCIGIAG 68
OY 53 -IVGTSSFLKKVGSILGKRIISLWGLFPFSGSTNIMODILRETOFANRLNTDTLA 111
DB 69 KILGLGVPPAGVAVSLY-SFLIGELM-----PKGK-NQMEIFMEHVEIINQKISTARN 122
OY 112 RVNAELGLOANIREFNOQVDFNPNTQNPVLSTT-SSVNTMOQLFLNRLPOFRVQYQ 170
DB 123 KALTDKLGIDALAVVHDSLESVWGNRRNTARASVQYALIELMFVQGLDSFVASEE 182
OY 171 LLLLPLFAQANMHSIFRDVVLNADENGISAATLRTQYQYKNTTYSVNCINTYOTA 230
DB 183 VPLPIYAQANLHLLILDASIFGKEWGLSSSEISTFYRQVBERADYSYHCVKWTSG 242
OY 231 FRGL-NTRLHDMU---EFFTYMFLNVEFVYSIMSLFKYQSLVSSGANL---YASGSGP 282
DB 243 LNNLRGTMASVWVRNQFRDMDTLNVLVDLVALPSPYDTQWPIKTTAQLTREYVTDALGT 302

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QY 283 QOIO-SFTSQDW-----PFL-----YSLFOVNSN-YVINGFSG 313
 DB 303 VHPSPSTSTWYNNAPSSAIEAAVVRNPHLDPLEQVYISLISMSNSTQYNNMMWG 362
 QY 314 ARLTQFPNIGLPGTTTHALLAAVNVSSGVSDIGAVFNQNSCSTFLPPLTPPV 373
 DB 363 HKL--BFTIGGTLANIST-----QSTNTSINPTLPFT 394
 QY 374 RSLWDSGDRGCVNTVT-----NMO--TESFESTLGRCAFTARGNSYFPD 419
 DB 395 SRDYRTESLAGNLFLOPVNGVPRVDHMFVTHPIAS-----DNFYPP 441
 QY 420 YFIRNISGVLVVRNEDLRPLHNEIRIESPGSTGRLAMVSVNRKNNYA-VHE 478
 DB 442 Y-----AGTGTQLOQSENEPPEATQPPYESHRSIIG--LISASVKAIVYSWTR 494
 QY 479 NGMTIHABEDYTGTTSPHATOV-----NQRTFISEKFG--NOGDSLPFOSNTYA 531
 DB 495 SA-----DRTN-TIEPNSITQIPVKAFLSSGAAVRGFGTGDILR--RTVGT 543
 QY 532 RYLRGNGN-----SYMLYLRVSLGNSRTIRVTNGRVYASVNVNTNNGVNDGARF 586
 DB 544 RQIRVNIINPPAQRVVRKRVASTTDLOHTSINGALINQNSFATMR-----GED 596
 QY 587 LDINMGVYASDNTNVPDINTV-----FNSGTQFELNINVEPTNL 628
 DB 597 LDYKTFRTVGTTPESFLDVOSTFTIGAMNFSQNEVYIDRIEFVPEV 645

RESULT 8

140590
 CRYV465 protein - *Bacillus thuringiensis*
 C.Species: *Bacillus thuringiensis*
 C.Date: 12-Aug-1996 #sequence, revision 12-Aug-1996 #ext_change 26-Aug-1999
 C.Accession: 140590
 R.Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.
 Appl. Environ. Microbiol. 61, 2402-2407, 1995
 A>Title: Distribution of cryV-type insecticidal protein genes in *Bacillus thuringiensis* tomocoids.
 A.Reference number: 139814; MUID:95314293; PMID:7793360
 A.Accession: 140590
 A.Status: preliminary; translated from GB/EMBL/DBJ
 A.Molecule type: DNA
 A.Residues: 1-719 <RES>
 A.Cross-references: EMBL:U07642; NID:g467234; PIDD:AAA82114.1; PID:g467235
 C.Genetics:
 A:Gene: cryV465
 C:Superfamily: parasporal crystal protein

Query Match 9.4%; Score 310.5; DB 2; Length 719;
 Best Local Similarity 22.7%; Pred. No. 3.1e-13;
 Matches 153; Conservative 116; Mismatches 259; Indels 145; Gaps 34;
 QY 27 EHSKSDTRKEMWEMKRTDHSLYVA-PIVGVSSFLKKVGSLLGKRISELWGLFFPG 85
 DB 47 EHSKSDTRKEMWEMKRTDHSLYVA-PIVGVSSFLKKVGSLLGKRISELWGLFFPG 85
 QY 86 STNLMQDILRETEQFLNORLNTDILARVNAELBGLQANTREFNQVDNPLNPTQNPVLS 145
 DB 98 KSO-WELFMEHVEEIIINOKITLYANRKLSDLGADLALAVHESLWVENNNTARRAS 156
 QY 146 IT-SGVNMOQLFLNLRPOFVVOGYQLLLPLFAQANNEHSFTRDVVLVADWIGISAT 204
 DB 157 VVKNGYALBELMFQGLPFAVSGEVPILPIYAAANHLILRLDSDSTGKMGUSASE 216
 QY 205 LATQNYKATYTTESYNCINTYOTA--FRGLNTELDHML-ERTYMLNVEEVSIMS 260
 DB 217 ISTFNKQVETRDYDHCICIKYVNTGNLNLKGNNAKSVRYORFKQMTLMLVDLVALEP 276
 QY 261 LEKXQSL--VSSGANL-----YASGSGP--QOTQSFTSQDWPLVSLPQVSNVNLGSG 313
 DB 277 --SYDLTVYPIKTTISQLTREVVTAIGVHPNQAFASTW-----YNNAPSSALE 326

QY 314 ARLTQFPNIGLPGTTTHALLA-----ANVYSGG--VSSGDIQAVFNQNSCSTFLP 366
 DB 327 AAIVIS--PHLDPLEKTKYISLSRWSNSTQYNNMMWGSHLEPPLGALNT----- 376
 QY 367 PLTPFVPSWLDGSDRGVNTVNMOTESP-----ESTLAGCAFTARGNSYFP 418
 DB 377 -----STQSTNTSINPTLPQTSRDVYRTESLAGNL----- 409
 QY 419 DYFIRNISGV-----LVNNEHLARPLHY-----NEIRNES--PSGTPG-- 457
 DB 440 -FLTPVNGVVRVDHMFKEPPLPIASDN-----FYGYAGVGTQLOQSENEPPEYTGQ 464
 QY 458 GLRAY-----WVSVNRKNNYA--VHNGMTIHABEDYTGTTSPHATOV----- 503
 DB 465 NYESYSHRISHIGLISASHVKALVYSWTRSA-----DRTN-TIEPNSITQIPVKA 515
 QY 504 -NNORRTFISEKFG--NOGDSLPFOSNTYARLYRGNGN-----SYMLYLRVSLGNSRT 556
 DB 516 FLSSGAAVVRGFGTGDILR--RINTGTGDIRVINPPAQRVVRKRVASTTDLOF 573
 QY 557 RVTNGRVYASVNTNNTNNGVNDGARFPLDINMGVYASDNTNVPDINTV--TFNSGTQ 615
 DB 574 HYSINGKALINQNSFATMR--GEDLDYKTFRTIGFTTPESFDVOSTFTIGAMNFSQNE 632
 QY 616 FELNINVEPTNL 628
 DB 633 VVIDRIEFVPEV 645

RESULT 9

549247
 parasporal crystal protein cry9Ca1 [validated] - *Bacillus thuringiensis*
 N.Alternate names: parasporal crystal protein cry7H
 C.Species: *Bacillus thuringiensis*
 C.Date: 01-Dec-2000 #sequence, revision 01-Dec-2000 #ext_change 01-Dec-2000
 C.Accession: A59350, S49247
 R.Lambert, B.; Buyse, L.; Decock, C.; Jansens, S.; Pijns, C.; Saey, B.; Saurinck, J.; V. Appl. Environ. Microbiol. 62, 80-86, 1996
 A>Title: A *Bacillus thuringiensis* insecticidal crystal protein with a high activity against *Spodoptera frugiperda* larvae.
 A.Reference number: A59350; MUID:96141404; PMID:8572715
 A.Accession: A59350
 A.Molecule type: DNA
 A.Residues: 1-1157 <LAM>
 A.Cross-references: EMBL:Z7527; NID:g547554; PIDD:CAA85764.1; PID:g547556
 A:Experimental source: several colworts
 C:Comment: This parasporal crystal protein, active against corn borer and other insects, C:superfamily: parasporal crystal protein
 C:keywords: delta-endotoxin

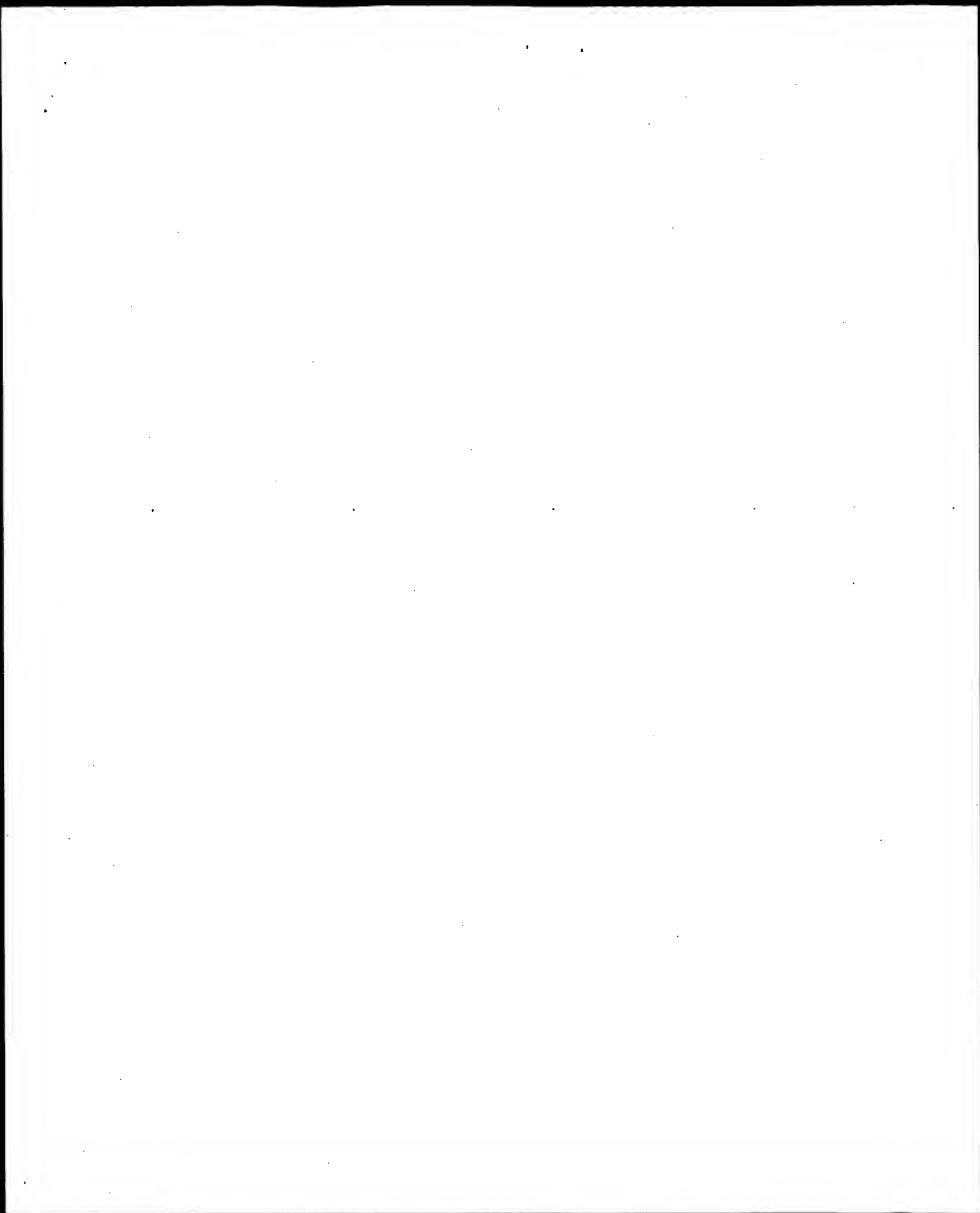
Query Match 9.3%; Score 307; DB 1; Length 1157;
 Best Local Similarity 23.4%; Pred. No. 1.1e-12;
 Matches 163; Conservative 87; Mismatches 215; Indels 232; Gaps 34;
 QY 52 PIVGVSSFLKKVGSLLGKRISELWGLFFPGSTNLMQDILRETEQFLNORLNTDILA 111
 DB 87 PFGQIVSFY-----QFLANTLW-----PVNDTAIWEAFNRQVEBLVNOQITEPARN 133
 QY 112 RVNAELGLOANIREFNOQVDFL--NPTQNPVPLSTSSVNTMOQL-FLNRRLPQRFVQ 167
 DB 134 QALRLQGLDGFNNYQBSLONMLABRNTN--LSVVRQAOTLADLDFVNALEFVAVN 190
 QY 168 GYQILLPLFAQANNEHSFTRDVVLNADWIGISATLFTYQNYLKNYTTESYNCINTY 227
 DB 191 GQOVPLISYVAQAVNHLILKQASLFGCGMGFTGSEISTYRQLELTAKYNTWCETWY 250
 QY 228 QTA--FRGLNT-----RLHDLREFTYMLNVEEVSIMSIFKXGSLVSSGANLVASG 280
 DB 251 NTGDLRLRGNTESLARKH--QREKEMTLVLDV--ALFFYDYV-----RLYFPGS 298
 QY 291 GPQQTQS--FTS-----QW-----FLY-----S 298
 DB 299 NPQLTREYVTDPIVENPPANVGLCRKMGTPYNTFSELENAFIRPHLEDRINGSLTSSN 358

Fri Aug 15 11:51:36 2003

us-10-040-906a-2.rpr

Page 9

Search completed: August 14, 2003, 18:12:44
Job time : 29 secs



GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 14, 2003, 18:08:22 ; Search time 15 seconds
(without alignments)
1981.392 Million cell updates/sec

Title: US-10-040-906a-2

Perfect score: 3314
Sequence: 1 MNVVLNGRTTICDANVVA.....GTQFELNMFVPTNLPTIY 632

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3048.5	92.0	633	1 C2AA_BACTK	P21253 bacillus th
2	3010.5	90.8	633	1 C2AB_BACTK	P21254 bacillus th
3	2916.5	88.0	633	1 C2AD_BACTU	O9rmg3 bacillus th
4	2545	76.8	622	1 C2AC_BACTU	O45743 bacillus th
5	1087	32.8	675	1 C1BA_PABPP	P57091 paenibacill
6	1080	32.6	706	1 C1AA_PABPP	O45358 paenibacill
7	1073.5	32.4	695	1 C1CA_PABPP	P57092 paenibacill
8	336.5	10.2	643	1 C2AA_BACTI	P21256 bacillus th
9	327.5	9.9	719	1 C1IA_BACTK	O45752 bacillus th
10	327.5	9.9	1231	1 C1BD_BACTZ	O9za25 bacillus th
11	325	9.8	719	1 C1ID_BACTU	O9xd11 bacillus th
12	310.5	9.4	719	1 C1IB_BACTE	O45709 bacillus th
13	307	9.3	1157	1 C9CA_BACTO	O45723 bacillus th
14	306	9.2	1138	1 C7AB_BACTA	O45707 bacillus th
15	305.5	9.2	1227	1 C1BE_BACTU	O85805 bacillus th
16	304.5	9.2	750	1 C8BB_BACTV	O9z105 bacillus th
17	300.5	9.1	682	1 C1BA_BACTH	O86170 bacillus th
18	294.5	8.9	1176	1 C1CB_BACTG	P56953 bacillus th
19	293.5	8.9	1229	1 C1BB_BACTU	O45729 bacillus th
20	293.5	8.9	1233	1 C1BC_BACTM	O45774 bacillus th
21	291.5	8.8	1179	1 C1AD_BACTA	O03744 bacillus th
22	288.5	8.7	1138	1 C7AB_BACTK	O45708 bacillus th
23	287	8.7	724	1 C8BA_BACTU	O45730 bacillus th
24	282.5	8.5	1169	1 C8BA_BACTK	O45705 bacillus th
25	280	8.4	1169	1 C9DA_BACTP	O06010 bacillus th
26	277	8.4	1181	1 C1AE_BACTL	O03748 bacillus th
27	275.5	8.3	1170	1 C1JB_BACTU	O45779 bacillus th
28	275.5	8.3	1228	1 C1BA_BACTK	P05517 bacillus th
29	273	8.2	1215	1 C1KA_BACTM	O45715 bacillus th
30	272.5	8.2	826	1 C8AA_BACTH	O98597 bacillus th
31	271.5	8.2	1176	1 C1AA_BACTK	P03265 bacillus th
32	270.5	8.2	1174	1 C1EB_BACTA	O03745 bacillus th
33	268	8.1	1155	1 C1AB_BACTK	P06578 bacillus th

34	267.5	8.1	1178	1 C1AC_BACTK	P05068 bacillus th
35	266	8.0	1167	1 C1JA_BACTU	O45738 bacillus th
36	265	8.0	1174	1 C1FA_BACTA	O03746 bacillus th
37	264.5	8.0	1160	1 C8CA_BACTP	O45706 bacillus th
38	261.5	7.9	1172	1 C1HA_BACTU	O45748 bacillus th
39	261	7.9	1169	1 C1FB_BACTM	O66377 bacillus th
40	260.5	7.9	1163	1 C0QA_BACTV	O9x597 bacillus th
41	259	7.8	1165	1 C1DA_BACTA	P19415 bacillus th
42	258.5	7.8	1176	1 C1AG_BACTU	O98515 bacillus th
43	255.5	7.7	649	1 C3CA_BACTK	O45744 bacillus th
44	253	7.6	1138	1 C7AA_BACTU	O03749 bacillus th
45	253	7.6	1150	1 C9EA_BACTA	O9znl9 bacillus th

ALIGNMENTS

RESULT 1
ID C2AA_BACTK STANDARD: PRT: 633 AA.
AC P21253.052764;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cry2aa (insecticidal delta-endotoxin
DE CryIIa(a)) (crystalline entomocidal protoxin) (71 kDa crystal protein)
DE (P2 crystal protein) (Mosquito factor).
GN CRY2AA OR CRYIIA(A) OR CRYBI OR CRYII.
OS Bacillus thuringiensis (subsp. kurstaki), and
OS Bacillus thuringiensis (subsp. keryae).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339, 33930;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=HD-1;
RX MEDLINE=89123178; PubMed=2914879;
RA Widner W.R., Whiteley H.R.;
RT "Two highly related insecticidal crystal proteins of Bacillus
RT thuringiensis subsp. kurstaki possess different host range
RT specificities.";
RL J. Bacteriol. 171:965-974(1989).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-26.
RC SPECIES=B.t.kurstaki; STRAIN=HD-263, and HD-1;
RX MEDLINE=88087146; PubMed=3121615;
RA Donovan W.P., Dankosik C.C., Gilbert M.P., Gawron-Burke M.C.,
RT "Amino acid sequence and entomocidal activity of the P2 crystal
RT protein. An insect toxin from Bacillus thuringiensis var. kurstaki.";
RL J. Biol. Chem. 263:561-567(1988).
RN [3]
RP REVISIONS.
RA Donovan W.P., Dankosik C.C., Gilbert M.P., Gawron-Burke M.C.,
RA Grost R.G., Carlton B.C.;
RL J. Biol. Chem. 264:4740-4740(1989).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.keryae; STRAIN=4A4C / HD-549;
RA Misra H.S., Khairnar N.P., Mathur M., Domally R.J., Mahajan S.K.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
-1- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
EPITHELIAL CELLS OF BOTH DIPTERAN (ADES AEGYPTI) AND LEPIDOPTERAN
(MANDUCA SEXTA) LARVAE.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
SPOROULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
OF THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
N-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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CC -----
DR EMBL; M23723; AAA83516.1; -
DR EMBL; M31738; AAA22335.1; -
DR EMBL; AF047038; AAC04867.1; -
DR PIR; C32053; C32053.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
KW Toxin; Sporulation.
FT VARIANT 1 MISSING (IN 50% OF THE MOLECULES).
FT VARIANT 3 N -> S (IN STRAIN 4A4C / HD-549).
FT VARIANT 409 F -> S (IN STRAIN 4A4C / HD-549).
FT VARIANT 541 S -> S (IN STRAIN 4A4C / HD-549).
FT VARIANT 588 S -> P (IN STRAIN 4A4C / HD-549).
SQ SEQUENCE 633 AA; 70852 MW; 15182F4C77858A4 CRC64;

Query Match 92.0%; Score 3048.5; DB 1; Length 633;
Best Local Similarity 90.7%; Pred. No. 3.2e-198;
Matches 574; Conservative 34; Mismatches 24; Indels 1; Gaps 1;

QY 1 MNNVANGRTTICDANYVAADPFSEFKSLDTIRKEMEMKRTDHSLYVAVIGVSSF 60
Db 1 MNNVANGRTTICDANYVAADPFSEFKSLDTIRKEMEMKRTDHSLYVAVIGVSSF 60
QY 61 LKRVGSLIGKRIILSELMGLIFPSSGNTLMODILRETEQFLNQRLNTDTLARVAALBEL 120
Db 61 LKRVGSLIGKRIILSELMGLIFPSSGNTLMODILRETEQFLNQRLNTDTLARVAALBEL 120
QY 121 QANIEFNOQVDFNFTQNPVPLSTSSVNTWQQLFRLDPQFVQVQQLLLPFAQA 180
Db 121 QANIEFNOQVDFNFTQNPVPLSTSSVNTWQQLFRLDPQFVQVQQLLLPFAQA 180
QY 181 ANNHLSFTRDVYLNADKMGISAATLTQNTLKRKTYEVSNCITTYTAFARGLNRLD 240
Db 181 ANNHLSFTRDVYLNADKMGISAATLTQNTLKRKTYEVSNCITTYTAFARGLNRLD 240
QY 241 MLEFRTYFNLVFEYVINSLEPKYQSLVSSGANTVASSGPGQOTOSTSQDMPFLYSLF 300
Db 241 MLEFRTYFNLVFEYVINSLEPKYQSLVSSGANTVASSGPGQOTOSTSQDMPFLYSLF 300
QY 301 QVNSVYVNGFSGARLTQFPNIGLPGTTTHLLAAVNSGVSQSGDIGAV-PNOVF 359
Db 301 QVNSVYVNGFSGARLTQFPNIGLPGTTTHLLAAVNSGVSQSGDIGAV-PNOVF 359
QY 360 SCSTPLPLLPFVRSWLDGSDRGVNTVNMQTESFESTLGLRCGAFARQNSVYFPD 419
Db 361 SCSTPLPLLPFVRSWLDGSDRGVNTVNMQTESFESTLGLRCGAFARQNSVYFPD 419
QY 420 YFIRNIGSVPLVYVNEDELRRPLHYEINIESPBGPGGLRAVYVNSKRNIVYVHN 479
Db 421 YFIRNIGSVPLVYVNEDELRRPLHYEINIESPBGPGGLRAVYVNSKRNIVYVHN 479
QY 480 GFMHILAPEDYTGFTTSPHATQVNNQRTFISERTGNGGDSLRFESQNTTARYLKNG 539
Db 481 GFMHILAPEDYTGFTTSPHATQVNNQRTFISERTGNGGDSLRFESQNTTARYLKNG 539
QY 540 NSGNLYLRVSSLGNSITRTVINGRYVYTSNNNTTNDVNDVNGARFSDINIGRYVASN 599
Db 541 NSGNLYLRVSSLGNSITRTVINGRYVYTSNNNTTNDVNDVNGARFSDINIGRYVASN 599
QY 600 TAVPLDINVTNPGTOEELNIMETVNTLPPIY 632
Db 601 TAVPLDINVTNPGTOEELNIMETVNTLPPIY 632

RESULT 2
C2AB_BACTK STANDARD; PRT; 633 AA.
ID_C2AB_BACTK

AC P21254;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cry2ab (insecticidal delta-endotoxin
DE CryIIA (b)) (crystalline entomocidal protoxin) (71 kDa crystal protein).
GN CR2AB OR CRYIIA(B) OR CRY2B.
OS Bacillus thuringiensis (subsp. kurstaki).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NC NCBI_TaxID=23339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-1;
EX MEDLINE=89123178; PubMed=2914879;
RA Widner W.R., Whiteley H.R.;
RT "Two highly related insecticidal crystal proteins of Bacillus
RT thuringiensis subsp. kurstaki possess different host range
RT specificities."
RL J. Bacteriol. 171:965-974 (1989).
RN [2]
RP SEQUENCE FROM N.A.
EX MEDLINE=91211618; PubMed=2089222;
RA Dankocsk C.C., Donovan W.P., Jany C.S.;
RT "Activation of a cryptic crystal protein gene of Bacillus
RT thuringiensis subspecies kurstaki by gene fusion and determination of
RT the crystal protein insecticidal specificity."
RL Mol. Microbiol. 4:2087-2094 (1990).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BTC002;
RA Chen Z.Y., Huang D.F.;
RT "Bacillus thuringiensis Btc002 cry2ab gene."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC - FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF LEPIDOPTERAN (MANDUCA SEXTA) LARVAE.
CC - DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOROGATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC - MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC - SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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CC EMBL; M23724; AAA22342.1; -
CC EMBL; X55416; CAA39075.1; -
CC EMBL; AF164666; AAG36762.1; -
CC PIR; D32053; D32053.
CC InterPro; IPR005638; endotoxin_C.
CC InterPro; IPR005639; endotoxin_N.
CC Pfam; PF03944; endotoxin_C; 1.
CC Pfam; PF03945; endotoxin_N; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 633 AA; 70741 MW; 424B937DFDDF3D61 CRC64;

Query Match 90.8%; Score 3010.5; DB 1; Length 633;
Best Local Similarity 89.7%; Pred. No. 1.2e-195;
Matches 568; Conservative 39; Mismatches 25; Indels 1; Gaps 1;

QY 1 MNNVANGRTTICDANYVAADPFSEFKSLDTIRKEMEMKRTDHSLYVAVIGVSSF 60
Db 1 MNNVANGRTTICDANYVAADPFSEFKSLDTIRKEMEMKRTDHSLYVAVIGVSSF 60
QY 61 LKRVGSLIGKRIILSELMGLIFPSSGNTLMODILRETEQFLNQRLNTDTLARVAALBEL 120
Db 61 LKRVGSLIGKRIILSELMGLIFPSSGNTLMODILRETEQFLNQRLNTDTLARVAALBEL 120

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QY 121 QANIREFNOQVDNFMPTONPVPPLSTTSVNTMOQLFLNRLPFRVOGYQLLLPLFAQA 180
DB 121 QANVEEFNRQVDNFMPTONPVPPLSTTSVNTMOQLFLNRLPFRVOGYQLLLPLFAQA 180
QY 181 ANMHLSFIRDVYLANDEMGISAATLTQNTYKATTEYSNVCINTYQTAARGANTRLHD 240
DB 181 ANMHLSFIRDVYLANDEMGISAATLTQNTYKATTEYSNVCINTYQTAARGANTRLHD 240
QY 241 MLEFRTYMFANVEEYVSIWLSFKYQSLVSSGANLYASGSGPOQTOSTFSDMPFLYSLF 300
DB 241 MLEFRTYMFANVEEYVSIWLSFKYQSLVSSGANLYASGSGPOQTOSTFSDMPFLYSLF 300
QY 301 QVANSNYLVNGFSGARLTOTFPNIGLPGTTTHALLAARVNSGSGSDI-GA-VERONF 359
DB 301 QVANSNYLVNGFSGARLTOTFPNIGLPGTTTHALLAARVNSGSGSDI-GA-VERONF 359
QY 360 SCSTFLPPLLPFVRSWLDGSDRGVNTVNTMOTESFESTLGLRCGAFARGNSNYPD 419
DB 360 SCSTFLPPLLPFVRSWLDGSDRGVNTVNTMOTESFESTLGLRCGAFARGNSNYPD 419
QY 420 YFIRNISGVPLVVRNEDLRPLHAYNEIRNISPSGTPGGLAAYVNSHKNKIYAVHEN 479
DB 420 YFIRNISGVPLVVRNEDLRPLHAYNEIRNISPSGTPGGLAAYVNSHKNKIYAVHEN 479
QY 480 GTMHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFQSNNTTARTYLRGNG 539
DB 480 GTMHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFQSNNTTARTYLRGNG 539
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DB 540 NSYNLYRVSSLGNSITRVINGRYVTASNVNTTNDGNGNGARFLDIMGVAVASDN 599
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DB 600 TNPVPLDINTVNSGTQPELMNIMFVPTNLPPLY 632
QY 601 SDVPLDINTVNSGTQPELMNIMFVPTNLPPLY 633
DB 601 SDVPLDINTVNSGTQPELMNIMFVPTNLPPLY 633

RESULT 3
C2AC BACTU STANDARD; PRT; 633 AA.
AC 09RMG3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cry2Ad (Insecticidal delta-endotoxin
DE CryIIA(d) (Crystalline entomocidal protoxin) (71 kDa crystal protein).
GN CRY2AD OR CRYIIA(D) OR CRY2.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=1428;
RN [1]
RP SEQUENCE FROM N.A.

RA Choi S.-K., Shin B.-S., Park S.-H.;
RT "Nucleotide sequence of a new Bacillus thuringiensis cry2-c-type gene."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPIITHELIAL CELLS OF INSECTS.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOREULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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DR EMBL: AF200816; AAF0563.1; -.
DR InterPro: IPR005638; endotoxin_C.
DR InterPro: IPR005639; endotoxin_N.
DR Pfam: PF03944; endotoxin_C_1.
DR Pfam: PF03945; endotoxin_N_1.
DR Toxin: Sporulation.
SQ SEQUENCE 633 AA; 70752 MW; 2A582067131B93CB CRC64;

Query Match      88.0%; Score 2916.5; DB 1; Length 633;
Best Local Similarity 87.2%; Pred. No. 2,5e-189;
Matches 552; Conservative 44; Mismatches 36; Indels 1; Gaps 1;

QY 1 MNNVLANNGRTTCDAYNVVADHPFSEFHKSLDTRKEMEMKRTDHSIYVAPVIGTVSSF 60
DB 1 MNSVANSGRNTCDAYNVVADHPFSEFHKSLDTRKEMEMKRTDHSIYVAPVIGTVSSF 60
QY 61 LKKYKGLIGKRLISLNLGLIPSGSTNMEDILRTEKFLNQLKNTDLSRVNAELTGL 120
DB 61 LKKYKGLIGKRLISLNLGLIPSGSTNMEDILRTEKFLNQLKNTDLSRVNAELTGL 120
QY 121 QANIREFNOQVDNFMPTONPVPPLSTTSVNTMOQLFLNRLPFRVOGYQLLLPLFAQA 180
DB 121 QANVEEFNRQVDNFMPTONPVPPLSTTSVNTMOQLFLNRLPFRVOGYQLLLPLFAQA 180
QY 181 ANMHLSFIRDVYLANDEMGISAATLTQNTYKATTEYSNVCINTYQTAARGANTRLHD 240
DB 181 ANMHLSFIRDVYLANDEMGISAATLTQNTYKATTEYSNVCINTYQTAARGANTRLHD 240
QY 241 MLEFRTYMFANVEEYVSIWLSFKYQSLVSSGANLYASGSGPOQTOSTFSDMPFLYSLF 300
DB 241 MLEFRTYMFANVEEYVSIWLSFKYQSLVSSGANLYASGSGPOQTOSTFSDMPFLYSLF 300
QY 301 QVANSNYLVNGFSGARLTOTFPNIGLPGTTTHALLAARVNSGSGSDI-GA-VERONF 359
DB 301 QVANSNYLVNGFSGARLTOTFPNIGLPGTTTHALLAARVNSGSGSDI-GA-VERONF 359
QY 360 SCSTFLPPLLPFVRSWLDGSDRGVNTVNTMOTESFESTLGLRCGAFARGNSNYPD 419
DB 360 SCSTFLPPLLPFVRSWLDGSDRGVNTVNTMOTESFESTLGLRCGAFARGNSNYPD 419
QY 420 YFIRNISGVPLVVRNEDLRPLHAYNEIRNISPSGTPGGLAAYVNSHKNKIYAVHEN 479
DB 420 YFIRNISGVPLVVRNEDLRPLHAYNEIRNISPSGTPGGLAAYVNSHKNKIYAVHEN 479
QY 480 GTMHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFQSNNTTARTYLRGNG 539
DB 480 GTMHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFQSNNTTARTYLRGNG 539
QY 540 NSYNLYRVSSLGNSITRVINGRYVTASNVNTTNDGNGNGARFLDIMGVAVASDN 599
DB 540 NSYNLYRVSSLGNSITRVINGRYVTASNVNTTNDGNGNGARFLDIMGVAVASDN 599
QY 600 TNPVPLDINTVNSGTQPELMNIMFVPTNLPPLY 632
DB 600 TNPVPLDINTVNSGTQPELMNIMFVPTNLPPLY 632
QY 601 SDVPLDINTVNSGTQPELMNIMFVPTNLPPLY 633
DB 601 SDVPLDINTVNSGTQPELMNIMFVPTNLPPLY 633

RESULT 4
C2AC BACTU STANDARD; PRT; 622 AA.
AC 045743;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cry2Ac (Insecticidal delta-endotoxin
DE CryIIA(c) (Crystalline entomocidal protoxin) (70 kDa crystal protein).
GN CRY2AC OR CRYIIA(C) OR CRYIIC.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=1428;
RN [1]
RP SEQUENCE FROM N.A.

```

RC STRAIN=Shanghai 1 / S-1;
 RX MEDLINE=91340086; PubMed=1651878;
 RA Wu D., Cao X.L., Bai Y.Y., Aronson A.I.;
 RT "Sequence of an operon containing a novel delta-endotoxin gene from
 B. thuringiensis";
 RL B. thuringiensis. Lett. 65:31-36(1991).
 CC PEMS Microbiol. Lett. 65:31-36(1991).
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPIHELIAL CELLS OF LEPIDOPTERAN LARVAE. HAS LOW ACTIVITY ON
 CC DIPTERAN LARVAE.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPORE FORMATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X57252; CAA04536.1; -
 CC DR PIR; S17402; S17402.
 CC DR InterPro; IPR005638; endotoxin_C.
 CC DR InterPro; IPR005639; endotoxin_N.
 CC DR Pfam; PF03944; endotoxin_C_1.
 CC DR Pfam; PF03945; endotoxin_N_1.
 CC KW Toxin; Sporulation; Plasmid.
 CC SEQUENCE 622 AA; 69729 MW; E0B5FAD37BF6299 CRC64;
 SQ
 Query Match 76.8%; Score 2545; DB 1; Length 622;
 Best Local Similarity 78.9%; Pred. No. 2.9e-164;
 Matches 501; Conservative 45; Mismatches 73; Indels 16; Gaps 8;

QY 538 NGSNYLTVARSSLSGSTRITRTINGRVYATSNVNTTNDGVNDGARFDJIMGNVVAS 597
 DB 529 NGSNYLTVARSSLSGSTRITRTINGRVYATSNVNTTNDGVNDGARFDJIMGNVVAS 587
 QY 598 DNTNVPDIDINTNSGTOPELNMIFPTPLPIRY 632
 DB 588 ANTNPVLDIQTFNGNPOPELNMIFPTPLPIRY 622
 RESULT 5
 CIBA PAEP STANDARD; PRT; 675 AA.
 ID CIBA PAEP
 AC P57091;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Parasporal crystal protein cry18a (Parasporal delta-endotoxin
 DE CryXVIII(a)) (Crystalline parasporal protoxin) (76 kDa crystal
 DE protein).
 GN CRY18A OR CRYXVIII(a). (Bacillus popilliae).
 OS Paenibacillus popilliae (Bacillus popilliae).
 OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
 OX NCBI_TaxID=78057;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BP3;
 RA Patel R., Yousten A.A., Rippere K.;
 RT "Detection of two new cry genes in Paenibacillus popilliae";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: BINDS TO THE BRUSH BORDER MEMBRANE VESICLES OF SCAB
 CC LARVAE AND DAMAGES THE GUT WALL SOMEHOW TO ALLOW THE VEGETATIVE
 CC CELLS OF P. POPILLIAE TO ENTER THE HEMOLYMPH (BY SIMILARITY).
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPORE FORMATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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 CC -----
 CC EMBL; AF169250; AAF69667.1; -
 CC DR InterPro; IPR005638; endotoxin_C.
 CC DR InterPro; IPR005639; endotoxin_N.
 CC DR Pfam; PF03944; endotoxin_C_1.
 CC DR Pfam; PF03945; endotoxin_N_1.
 CC KW Toxin; Sporulation.
 CC FT DOMAIN 101 POLY-LEU.
 CC FT DOMAIN 199 204 POLY-LEU.
 CC SEQUENCE 675 AA; 75848 MW; 823B58B4A81D5 CRC64;
 SQ
 Query Match 32.8%; Score 1087; DB 1; Length 675;
 Best Local Similarity 38.9%; Pred. No. 7.3e-66;
 Matches 259; Conservative 104; Mismatches 244; Indels 58; Gaps 19;

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Db 206 AAGATLHLTFIDIIINAGENWIPERQNTCKRYKQVAVASVNAALSTYEGAFARARFP 265
Qy 235 NTRLDMLERFTYFELANFEYVSIWLSFKYQSLVAVSGANLVAASGPOQOTQSTQDWP 294
Db 266 RATLENNLOKTFMTLVNLDVSIWLSLKNMVLSTANLNYNGDKNKBEPHSISWIP 325
Qy 295 FLYSLQVNSNYVANGSGARLQTFPENGALPGITTHALLAARVNSGVSGDGAIV 354
Db 326 FENSYIQTNSNYVLSGVSGVIRWYKLT-FFGGYIODNMLNIIASVYGVNGPKIGVQ 383
Qy 355 FNO-----NFSCSTFLPPLLPFRSGMLDSGDRGVVTVYTW 392
Db 384 LSTTELDKQIKQAGARMPGTGDLSPNC-TLANFTYPRYACNPDELSTAGTGF 442
Qy 393 QTESFESTGLACGAFARGNS-NYPDFYFNISG-VPLVKNEDLRPLHNEIRNIE 450
Db 443 RSDVFSBEDNI-CGAGTGYASAMTSPDYIINISATVQVDGINDI-TPLCFGEDALIT 500
Qy 451 SPSCGTQGLRAYVSVNHRKNIIYAVHENGIMHLPEDYGFETISPIHATQVNNQRTF 510
Db 501 STHGIV-----NKVIAYNRKANLAGNONGMTIHQAPDGTFTVSLHLSFTHPEAH 555
Qy 511 ISEKFGNODSLRFGQSTTRKRYTLGNGNS-YNLYKAVS-LGNSTIRVITNGRYTAS 568
Db 556 IQENYVGSQDSLRTGPTTALTYMLSGDRRTYKLVKAVSGVITRTAKVRNSIGY-LE 614
Qy 569 NVATTTNDGVNDGARFLDINNGVAVASD-NTNVPDLINVTNFGSTQPELMNIMFPTN 627
Db 615 YINTVNDNGITDNSKRFQDEPRFITTDADPTIVLEFASIN-----FDLKNLIFIPY 670
Qy 628 LPPIY 632
Db 671 DTPY 675

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RESULT 6
CICA_PABP STANDARD; PRT; 706 AA.

AC 045358;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Parasporal crystal protein cry18aA (Parasporal delta-endotoxin
DE Cryxviii(a)) (Crystalline parasporal protoxin) (79 kDa crystal
protein)
GN CRYXVIII(A) OR CRYBP.
OS Paenibacillus popilliae (Bacillus popilliae).
OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
OX NCBI_taxid=78057;
RN (1)
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=H1 / subsp. melolonthae;
RX MEDLINE=97352693; PubMed=9209052;
RA Zhang J., Hodgman T.C., Krieger L., Schaefer W., Schaefer H.U.,
RT "Cloning and analysis of the first cry gene from Bacillus popilliae.",
RU J. Bacteriol. 179:4336-4341 (1997).
CC -I- FUNCTION: BINDS TO THE BRUSH BORDER MEMBRANE VESICLES OF SCARAB
CC LARVAE AND DAMAGES THE GUT WALL SOMEHOW TO ALLOW THE VEGETATIVE
CC CELLS OF P. POPILLIAE TO ENTER THE HEMOLYMPH. ACTIVE ON
CC M. MELOLONTA.
CC -I- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOREATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT (BY SIMILIARTY).
CC -I- SIMILIARTY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.

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DR EMBL; X99049; CAA67506.1; -.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF00555; endotoxin_1.
DR Pfam; PF03944; endotoxin_C_1.
DR Pfam; PF03945; endotoxin_N_1.
DR Toxin; Sporulation.
KW CONFLICT 670 670 T -> F (IN REF. 1; AA SEQUENCE).
SQ SEQUENCE 706 AA; 79034 MW; 9172B949BE499CID CRC64;

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Query Match 32.6%; Score 1080; DB 1; Length 706;
Best local similarity 38.4%; Pred. No. 2,36-65;
Matches 264; Conservative 96; Mismatches 233; Indels 94; Gaps 21;

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Qy 2 NNVLTNN-----GRTTICDA-----YNAVADPFSFHKSLDTRKEMWERTD 45
Db 58 NNDNNNDALCDELGLPIDNNITCSTDEPTINWVRDP--FKKSTQELTREMTWKENS 115
Qy 46 HSLYAPVGVVSSFLKKVGSIGKRTLSLMLFPBGSTNLMQDILRETPFLANQL 105
Db 116 PSLETPALGVAVISFLQSLKQATSFLLKTLDDLFPNNSSLMEILRATQVQERL 175
Qy 106 NTDTLARYNAELRGIQANIREFNOQVDNLPQNPVPLSTISSVNTVQQLFLARLPOR 165
Db 176 DDTANRVSQELVGLKNVLTTFNDQVEDFLQNRVGSPLAIIIDSLNTMQQLFVNRLPQR 235
Qy 166 VQCYQLLLPLPQAANMLHSLRIVVANDENGISAATLRYQNYLNTTRYSYCN 225
Db 236 VSGYVLLPLPQAATLHLPARDVIINDENNITFLQALNTYTYFKEYIAESVYALS 295
Qy 226 TYQTAFRGLNTR-----LHMLERFTYFELANFEYVSIWLSFKYQSLVAVSGANLYASG 279
Db 296 TYDQGR---TRFYPRVTLIEDMLQKTFMTLVNLDVSIWLSLKNMVLSTANLNYNG 352
Qy 280 SSGQQTQSFQDMPFLYSLFQVNSNYVANGSGARLQTFPENGALPGITTHALLAARVNSGVSGDGAIV 411
Db 353 DNKNREGAPVSYGPFENSTYQTKSNVYLSGVSGIGARFTYTVLGRYLDHDKNITTT- 411
Qy 334 ALLAARVNSGVSGDGAIVN-----ONFSCSTFLP-DLTP 371
Db 412 -----YVGQTGPGPIGVQSTTELDKQQAQTRDLSLVDFPFLIACMLPNRTAP 463
Qy 372 -FVRSMLSG-SDRGVNNTVMQRESFESTGL-RCGAFARGNSNFPDYRTIRISYV 428
Db 464 YRATSLVESRYSSIGYLRKDVFSK--DSTCGLNGPMWTS-----YDPYITNISAT 515
Qy 429 PLYVKNEDLRPLHNEIRNIESPSTGGILRAYVSVNHRKNIIYAVHENGIMHLP 488
Db 516 VQNGENTDTPLYFKENRPITSTRGV-----NKVIAYNRKANLAGNONGMTIHQAP 570
Qy 489 DYTGTISPIHATQVNNQRTFISEKRNQDGLRFGQSTTRKRYTLGNGNS-YNLYKAVS 547
Db 571 DDTGFTVSLPFA--NTTSTYKENGNSGDSLH--KQGYLAHMLSGNGQRYVLVR 627
Qy 548 VSLIAGNSTRTVINGRYTASNVNTTNDGVNDGARFLDINNGN--VVASDNTVNP 605
Db 628 LSGAAN---QIKQSLFTSIYAFDSTINNEGITDNSKRFQDEPRFITTDADPTIVLEFASIN-----E 679
Qy 606 INVTNFGSTQPELMNIMFVPTNLPPIY 632
Db 680 ILYVEGVSLDMLNLIPLADPTIVLY 706

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RESULT 7
CICA_PABP STANDARD; PRT; 695 AA.

AC P57092;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Parasporal crystal protein cry18aA (Parasporal delta-endotoxin
DE Cryxviii(a)) (Crystalline parasporal protoxin) (78 kDa crystal

```

DE  proteain.
GN  CRYI8CA OR CRYXIIIC(A).
OS  Paenibacillus popilliae (Bacillus popilliae).
OC  Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
OX  NCBI_TaxID=78057;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=ATCC 14706;
RA  Patel R., Yonsten A.A., Rippe K.;
RT  "Detection of two new cry genes in Paenibacillus popilliae.";
RL  Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC  -1- FUNCTION: BINDS TO THE BRUSH BORDER MEMBRANE VESICLES OF SCARAB
CC  LARVAE AND DAMAGES THE GUT WALL, SOMEHOW TO ALLOW THE VEGETATIVE
CC  CELLS OF P. POPILLIAE TO ENTER THE HEMOLYPH (BY SIMILARITY).
CC  -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC  SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC  OF THE SPORE COAT (BY SIMILARITY).
CC  -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; AF169251; AAR09668.1; -
DR  InterPro; IPR005638; endotoxin_C.
DR  InterPro; IPR005639; endotoxin_N.
DR  Pfam; PF03944; endotoxin_C_1.
DR  Pfam; PF03945; endotoxin_N_1.
DR  Toxin; Sporulation.
SQ  SEQUENCE 695 AA; 78259 MW; 406AC9154D75B070 CRC64;

Query Match      32.4%; Score 1073.5; DB 1; Length 695;
Best Local Similarity 37.6%; Pred. No. 6.2e-65;
Matches 256; Conservative 115; Mismatches 241; Indels 69; Gaps 18;

QY  2 NNV-----LNNGRITTCIDAY-----NVVAHDFSPFHKSLDITRKEMWKKTHDS 47
DB  34 NNVNNGDLVNTGILPINDNFGNGFIPRNVTRKDP--PRKATQEFIREMTWKKKAS 91
QY  48 LVVARIYGVTSSELLKKGKSLGKRIISELWGLFPGSGSTNMODIIRTEGPNORNT 107
DB  92 LFTAPIVEVITSTLELKKGLVAGKVLMSLNLNLFNNSTIMEELIATQYIQGLDT 151
QY  108 DTLARVNALEGLQANIREFNOQVDFLNPONPVPLSTSSVNTMOQLFNLDPQVRQ 167
DB  152 VTMNVRVQELGKLNDFLTFNQIDFLQNRVGISPLATIDISINTMOQLFVNLPQVQS 211
QY  168 GVOULLLPLFAQANMHLSPFDVYLNADENGLSALTFTQNTYNYKNYTEVENCINTY 227
DB  212 DDOVLLPLPFAQAVTLLHLPVBDITINADENLPBQALNTYKRYKQYVAQISNTYLSLY 271
QY  228 QTAFRG---LNTFLHMLEFTYVFLNVEEYVSIWSPKYQSLVSSGANTYASGSGPQ 283
DB  272 EEARFARFYPYRNT-VERMLEFKEFTPLNVLVDIVSMSSLLKYVNLVSTANLYNDKXY 330
QY  284 QTOSTFSDMPBELSLFQVNSVYLVNGSGARLQGFPR-----IGG 325
DB  331 NGEYSISYMPFENTYIYQTKSNYVLSGVSQWAMSWSTNPFGEYIQDHLNITASYIGG 390
QY  326 LFG-----TYYTALLARVNSGCVSSGDI GAVFNQNSCTPLPLPLPFVRSWL 377
DB  391 VNGPQIGQALSTELDQVQQ-----ARADIPVDFTQIPINCTLRNLEPVYATRF 443
QY  378 DSGSRGAVNTVMQTESFESTLGRGAT-ARGNSYVPDYINISIG-VELAVNRE 435
DB  444 NEUTSLGTVAGVGFSVSDVFNDSV-CGLGTVSSGQTFPYDYITNISAITYQVAGVYT 502
QY  436 DLRRLAHNEIRNIESPSGTGGRLAVVNSVNRKNIIYAVHN--GTMLHLPEDYTG 493

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DB  503 DI-SPLFGENRATISTNGV-----NKVIAIYNRKTN-YDDEFNIRGTVIHEAFSTG 555
QY  494 TISPIHATQVNNQNRFTISEKFGNQSDFRFGQNTTARVTL-RGNSNYLVYRVSSLG 552
DB  556 TISPELHDVTNNSYLYIQNYNANQDSLRV-INRAIKRLSARSRVYLVYRVSGTA 614
QY  553 NSTIRVTINGRVYTAENVNTTNDGVDNARFLDINMGVAVASDNTNVPLDINT-EN 611
DB  615 SSIYAIVENYVPGSANOINTGIDNEGVINDSKFIDIFNTPSVSGTARELOQVSGAT 674
QY  612 SGQFELANINMVEPTNPLPIY 632
DB  675 TSPEDIMIIILIPINDVPLX 695

RESULT 8
CBA_BACTI
ID CBA_BACTI STANDARD; PRT; 643 AA.
AC P21256;
DT 01-MAY-1991 (Rel. 18, last sequence update)
DT 01-MAY-2001 (Rel. 40, last annotation update)
DE Pepticidal crystal protein cryIIAa (insecticidal delta-endotoxin
DE cryIIAa) (crystalline entomocidal protoxin) (72 kDa crystal protein).
GN CRYIIA OR CRYXIIA(A) OR CRYIIV OR CRYD.
OS Bacillus thuringiensis (subsp. israelensis).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1430;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8908093; PubMed=2902069;
RA Donovan W.P., Dankocsi C.C., Gilbert M.P.;
RT "Molecular characterization of a gene encoding a 72-kilodalton
RT mosquito-toxic crystal protein from Bacillus thuringiensis subsp.
RT israelensis.";
RL J. Bacteriol. 170:4732-4738 (1988).
CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF MOSQUITOS.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M31737; AAA2352.1; -
DR PIR; A43647; A43647.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03945; endotoxin_N_1.
DR Toxin; Sporulation.
SQ SEQUENCE 643 AA; 72348 MW; 64CA35495409B74E CRC64;

Query Match      10.2%; Score 336.5; DB 1; Length 643;
Best Local Similarity 23.1%; Pred. No. 2.9e-15;
Matches 167; Conservative 98; Mismatches 257; Indels 201; Gaps 34;

QY  27 EHKSLDITRKEMWKKTHDSLY-----VAP---IVGVSSFLKKGSLIGRILSE 76
DB  2 EDSISDITLSIV-----NETDFPLVNNYETLEPTLALIVAVIADYLTALGKAAKAAFSK 57
QY  77 LMGILPSSGSTNLMODILRETEQFLNORLNTDTLAVNALEGLQANIREFNOQVDFNL- 135
DB  58 VLSLIFPGSGPATMKEKRTVEVETLIHQKLSQDRVMIINAEYRG-----ILEVSDVPDAVIX 113
QY  136 NPTQNPVPLSLSTSSVNTMOQLFN-----RLPQFRVQGYOLLPLPFAQANMHLSPFI 188

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DB 114 QGFTPA-----TAKGFLNLGALIGLITLPOFEVOTBEVSNALFTQWCTLHTLL 164
 QY 189 RDVVLNADNEMGISAATLTATYONIAKNTTEYSNCINWYQTA-FGLNTRLDMLFEFRV 247
 DB 165 KDGLLGASMGFTQADVDSFKLPNOXKVDYTRTLMEMYTEERGLCKSLKDLGTRRM 224
 QY 248 MFLNFEYVISTSLFKYQSLVSSGANLYASGSGPQOTGFTSQDMPFLYSLFOVNSN-- 305
 DB 225 CNLYVFPFAEAMSLMREYEGKLOSLSL-----WDVVGVSIFVANNEM 267
 QY 306 ----YVINGSGARLTQTPPNIGLPTTTTHALLAARVNSG-----GVSSGDICAV 355
 DB 268 GGLVYKLMGEVNOGLTTVKNY-----SFTNEPADIDARENIRGVHPIYDSSGLTWIG 323
 QY 356 N---QNFSGSTFLPLPLTPVBSMDSGSDGCVNYTYNQ----- 393
 DB 324 NGRTNNENPAD-----NNGNEIMEVRYTQFYQNPNEPIAPRDIINQTLTA 369
 QY 394 -----TESFESTL---GLRCAFTARGN-----SNY--FPDYFRINI 425
 DB 370 PABADLFFKNADINVKFTQWFQSTLYGNWIKLGYTLSSRGTLIPRYLAVDGYTRAI 429
 QY 426 SGVPLVVR---NEDLRPLMYNIRNIBSPG-----TPGLRMYVSVHAKNNIYA 475
 DB 430 SACPBGVSLAYNHDL-TTLTYNRI-EYDSPTENIIVGFAPDWTDF-----YSKKS---- 479
 QY 476 VHENGTMHLAPEDYGTFTSPHATOVNQTFTISEKQNGQD-SLRFGOS--WTTAR 532
 DB 480 -----HYLSETNDSYVIALQFAEVSQD-RSFLDPDQATGSIKFAFTISENAK 529
 QY 533 YTLRGNSNYLILYVSLGNSITRTINGVYASVNTTNNGVNDGAPFLDING 592
 DB 530 YSTRLN-TGFWTATRYKLI-----IRRVRYPL--PACIRVQONSNN---PMLGSFTA 578
 QY 593 NV-----VASDNTVPLDINV-FENGSTQFELMIMFY-----PTUL 628
 DB 579 NNPMPVDFVTDAFTFNDLITTSSTNALFSSISDSINGSEWVLSQFLVKSAPFTQI 638
 QY 629 PPI 631
 DB 639 NPI 641

RESULT 9
 C1A_BACTK STANDARD; PRT: 719 AA.
 AC 045752; P71092; 045750; 045751; 045756;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DB 16-OCT-2001 (Rel. 40, Last annotation update)
 DB Peptidicidal crystal protein cryIIa (insecticidal delta-endotoxin
 DE CryII(a)) (crystalline entomocidal protoxin) (81 kDa crystal protein).
 DB CRYIIA OR CRYII(A) OR CRYV OR CRYV1 OR CGCXYV.
 OS *Bacillus thuringiensis* (subsp. kurstaki).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 ON NCBI_TaxID=29339;
 RX STRAIN=DSIR732;
 RC MEDLINE=93298009; PubMed=8517758;
 RA Gleave A.P., Williams R., Hedges R.J.;
 RT "Screening by polymerase chain reaction of *Bacillus thuringiensis*
 RT characterizes for the presence of cryV-like insecticidal protein genes and
 RT characterization of a cryV gene cloned from *B. thuringiensis* subsp.
 RT kurstaki.";
 RL Appl. Environ. Microbiol. 59:1683-1687 (1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CHCC4835;
 RX MEDLINE=92269582; PubMed=1588820;
 RA Taylor R., Tippet J., Gibb G., Pells S., Pike D., Jordan L., Ely S.;
 RT "Identification and characterization of a novel *Bacillus thuringiensis*

RT delta-endotoxin entomocidal to coleopteran and lepidopteran larvae.";
 RL Mol. Microbiol. 6:1211-1217 (1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HD-1;
 RX MEDLINE=95314293; PubMed=7793960;
 RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.-T., Lee S.-T., Kim J.-I.;
 RT "Distribution of cryV-type insecticidal protein genes in *Bacillus*
 RT *thuringiensis* and cloning of cryV-type genes from *Bacillus*
 RT *thuringiensis* subsp. kurstaki and *Bacillus thuringiensis* subsp.
 RT entomocidal.";
 RL Appl. Environ. Microbiol. 61:2402-2407 (1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB88;
 RX MEDLINE=96178985; PubMed=8606196;
 RA Koesteloha K., Warren G.W., Mullins M., Mullins A.D., Palekar N.V.,
 RA Craig J.A., Koziel M.G., Estruch J.J.;
 RT "Cloning of a cryV-type insecticidal protein gene from *Bacillus*
 RT *thuringiensis*: the cryV-encoded protein is expressed early in
 RT stationary phase.";
 RL J. Bacteriol. 178:2141-2144 (1996).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=61;
 RA Selvapandiyan A., Bhattacharjee R.K.;
 RT "Isolation, cloning and expression of cryV gene.";
 RL Submitted (Oct-1996) to the EMBL/GenBank/DBD databases.
 CC -I- FUNCTION: PROMOTES COLITIDISMOTIC LISTS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF CERTAIN COLEOPTERAN AND LEPIDOPTERAN SPECIES.
 CC -I- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -I- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -I- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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 CC
 DR EMBL: M98544; AAA22354.1;
 DR EMBL: X62821; CAA4633.1;
 DR EMBL: I36338; AAC3699.1;
 DR EMBL: I49391; AAB00958.1;
 DR EMBL: Y08920; CAA70124.1;
 DR PIR: I39815; I39815.
 DR HSP: S25383; S25383.
 DR HSP: P02965; ICIY.
 DR InterPro: IPR001178; Endotoxin.
 DR InterPro: IPR005638; endotoxin_C.
 DR InterPro: IPR005639; endotoxin_N.
 DR Pfam: PF00555; endotoxin_1.
 DR Pfam: PF03944; endotoxin_C_1.
 DR Pfam: PF03945; endotoxin_N_1.
 DR Toxin; Sporulation.
 FT VARIANT 159 233 K -> R (IN STRAIN 61).
 FT VARIANT 233 233 D -> Y (IN STRAIN JHC4835 AND HD-1).
 FT VARIANT 443 443 A -> V (IN STRAIN AB88).
 FT VARIANT 711 712 KQ -> NE (IN STRAIN HD-1 AND 61).
 SQ SEQUENCE 719 AA; 81216 MW; 362756C25DAF5 CRC64;
 Query Match 9.9%; Score 327.5; DB 1; Length 719;
 Best Local Similarity 22.8%; Pred. No. 1.4e-14;
 Matches 162; Conservative 103; Mismatches 271; Indels 173; Gaps 32;
 21 HDPSPEHK-----SLDTIRKEM-MEMKRTDH-----SLY-VAP----- 52

Db 9 HOSSESSNAKYKISTDSLKNETDIELQINHEDCIKSEYENVEPVSASTIQTGICIAQ 68
 QY 53 -IVGTVSSFLKRVYSILGKRIILSELMGLIFPSGSTNIMODILRETEQFLNORLNTDTLA 111
 Db 69 KILGTIGVPAQVVASLY-SFLLGELM-----PKG-NOMELFMEHEEELINOKISTAYAR 122
 QY 112 RVAAELBEGLOANIREFNOQVDFLPTQNPVPLST-SYVNMQOULFNLPLPFRVQVQ 170
 Db 123 KALDLDKGDALAVYHDSIESVGNKNNTRASVVSQYTALELFWGLKPSRAVSGEE 182
 QY 171 LLLPLFPAOANMHLSPFRDVLNADENGISATLRTYONLYKNTTEYSNYCINTYQTA 230
 Db 183 VPLLPFYAOANMHLILLRDASIFGKEMGLSSSESTFYNRQVERAGDSDHCVMVYSTS 242
 QY 231 FRGL-NTRLHDL-----ERRTYMFLNFEYVSIWSLFFKQSLIVSSGANL---YASGSGP 282
 Db 243 LNNRGTAESWVRNPFRRDMLVLDLALFPSYDTQMPFKTTAQLREYVTDALGT 302
 QY 283 QQTQ-SFTSQDM-----PFL-----YSLFQVNSN-VYINGFSG 313
 Db 303 VHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLFLEQVTVYLSLSRMSNTQYNNMVG 362
 QY 314 ARLTQTFPNIIGLPETTTTHALLAARVNSGVSAGDIGNVNFNSCSTFLPPLTPPV 373
 Db 363 HRL--NFRITGTLNIST-----QSTNTSINVTLPPT 394
 QY 374 RSWLDGSGDRGVNVT-----NQ--TESFEFTGLRGCAFTAGNSNTPD 419
 Db 395 SRDVTRESLAGNLELTQPVNGVPRVDFHMFVHPPLAS-----DMFYPG 441
 QY 420 YFIRNTSGVLYVRNEDLRPLHYNELRNIESPGTGGDLAVYVSHRNKNTYA-VHE 478
 Db 442 Y-----AGITQLODSENELEPPEATQGPNTYESHRLSHIG-LIASHVKALVYSMTHR 494
 QY 479 NGTMHLAPEDYTGFTTTHALLAARVNSGVSAGDIGNVNFNSCSTFLPPLTPPV 531
 Db 495 SA-----DRTN-TIEPNSITQIPVKAFLNLSGAAVVRGPGFTGGDLA-RTNLTG 543
 QY 532 RYTLRGNGN-----SYNLYLRVSLGNSITRTYNGRYVYASNNVTNTNDGVNDGARF 586
 Db 544 RGDIRVNIINPPAQRIRKIRYASTDLOPHNSINKKALINGNSATNMR-----GED 596
 QY 587 LDIMKGVNVASDNTNVPDLINT-----FNSGTQFELNIMVPLNL 628
 Db 597 LDYKTFRTVGTTPSFSLDVOSTFTIGANMFSSGNEVYIDRIEFPVEV 645

RESULT 10
 ClBD_BACT2 STANDARD; PRT; 1231 AA.
 ID ClBD_BACT2 STANDARD; PRT; 1231 AA.
 AC Q9ZAZ5,
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pesticidal crystal protein cryIbd (insecticidal delta-endotoxin
 DE CryIbd(d) (crystalline entomocidal protoxin) (140 kDa crystal protein).
 GN CRYIbd OR CRYIbd OR CRYIbd OR CRYIbd.
 OS Bacillus thuringiensis (subsp. whanensis).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_Taxid=52024;
 RN [1]
 RP SEQUENCE FROM N. A.
 RC STRAIN=HD-525;
 RX MEDLINE=20153386; PubMed=10688690;
 RA Kuo W.-S., Lin J.-H., Tzeng C.-C., Kao S.-S., Chak K.-F.;
 RT Cloning of two new cry genes from Bacillus thuringiensis subsp.
 RT whanensis strain. J. 40:227-232(2000).
 RL Curr. Microbiol. 40:227-232(2000).
 CC - FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF LEPIDOPTERAN LARVAE. TOXIC TO PLOUTELLA
 CC XYLOSTELLA.
 CC - DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART

CC OR THE SPORE COAT.
 CC - MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC - SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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 CC or send an email to license@ebi.ac.uk).
 CC CC
 DR EMBL; U70726; AAD10292.1; -
 DR HSP; P02965; ICY.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; endotoxin_C.
 DR InterPro; IPR005639; endotoxin_N.
 DR Pfam; PF00555; endotoxin_1.
 DR Pfam; PF03944; endotoxin_C_1.
 DR Pfam; PF03945; endotoxin_N_1.
 DR Toxin; Sporulation.
 KW KM
 SQ SEQUENCE 1231 AA; 139654 MW; 129A0371CDBEBE32 CRC64;
 Query Match 9.9%; Score 327.5; DB 1; Length 1231;
 Best local similarity 23.3%; Pred. No. 2.9e-14;
 Matches 155; Conservative 101; Mismatches 249; Indels 161; Gaps 29;
 QY 52 PIVGVSSFLKRVYSILGKRIILSELMGLIFPSGSTNIMODILRETEQFLNORLNTDTLA 111
 Db 73 PFAQGLASFYSPVIG-----ELM---PFG-RDPWEILEHVBOLIRQOVTENTN 118
 QY 112 RVAAELBEGLOANIREFNOQVDFLPTQNPVPLSTSYVNMQOULFNLPLPFRVQVQ 170
 Db 119 TALARLEGGRGVSQALFETMLNDRDARSIIIEERYVALIEDITTYAIPFLIRNRE 178
 QY 171 LLLPLFPAOANMHLSPFRDVLNADENGISATLRTYONLYKNTTEYSNYCINTYQTA 230
 Db 179 VPLPMTYAOANMHLILLRDASIFGKEMGLSSSESTFYNRQVERAGDSDHCVMVYSTS 242
 QY 231 FRGL-NTRLHDL-----NFRITGTLNIST-----QSTNTSINVTLPPT 394
 Db 239 LNNRGTAESWVRNPFRRDMLVLDLALFPSYDTQMPFKTTAQLREYVTDALGT 302
 QY 283 QQTQ-SFTSQDM-----PFL-----YSLFQVNSN-VYINGFSG 313
 Db 299 TNAPSGFASTWNNNAPSFAIEAAVVRNPHLLFLEQVTVYLSLSRMSNTQYNNMVG 362
 QY 314 ARLTQTFPNIIGLPETTTTHALLAARVNSGVSAGDIGNVNFNSCSTFLPPLTPPV 373
 Db 359 HRL--NFRITGTLNIST-----QSTNTSINVTLPPT 394
 QY 374 RSWLDGSGDRGVNVT-----NQ--TESFEFTGLRGCAFTAGNSNTPD 419
 Db 395 SRDVTRESLAGNLELTQPVNGVPRVDFHMFVHPPLAS-----DMFYPG 441
 QY 420 YFIRNTSGVLYVRNEDLRPLHYNELRNIESPGTGGDLAVYVSHRNKNTYA-VHE 478
 Db 442 Y-----AGITQLODSENELEPPEATQGPNTYESHRLSHIG-LIASHVKALVYSMTHR 494
 QY 479 NGTMHLAPEDYTGFTTTHALLAARVNSGVSAGDIGNVNFNSCSTFLPPLTPPV 531
 Db 495 SA-----DRTN-TIEPNSITQIPVKAFLNLSGAAVVRGPGFTGGDLA-RTNLTG 543
 QY 532 RYTLRGNGN-----SYNLYLRVSLGNSITRTYNGRYVYASNNVTNTNDGVNDGARF 586
 Db 544 RGDIRVNIINPPAQRIRKIRYASTDLOPHNSINKKALINGNSATNMR-----GED 596
 QY 587 LDIMKGVNVASDNTNVPDLINT-----FNSGTQFELNIMVPLNL 628
 Db 597 LDYKTFRTVGTTPSFSLDVOSTFTIGANMFSSGNEVYIDRIEFPVEV 645

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Db      662 LEFTSTN 667

RESULT 11
C1ID BACTU STANDARD, PRT, 719 AA.
AC 09XDL1
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cryII (insecticidal) delta-endotoxin
DE CryII(d) (crystalline entomocidal protoxin) (81 kDa crystal protein).
GN CryII OR CryII (D) OR NCRVY.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OK NCBI_TaxID=1428;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=BR30;
RX MEDLINE=20374042; PubMed=10919402;
RA Choi S.-K., Shin B.-S., Kong E.-M., Rho H.M., Park S.-H.;
RT "Cloning of a new Bacillus thuringiensis cryII-type crystal protein
RT gene.", Microbiol. 41:65-69(2000).
RL -----
CC -I- FUNCTION: PROMOTES COLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE. ACTIVE ON PLUTELLA
CC XYLSTELLA AND ON BOMBYX MORI.
CC -I- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORIULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -I- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -I- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
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CC -----
DR EMBL; AF047579; AAD4366.1; -.
DR HSBP; P02965; 1CTY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF00555; endotoxin_1.
DR Pfam; PF03944; endotoxin_C_1.
DR Pfam; PF03945; endotoxin_N_1.
DR Toxin; Sporulation.
KW Toxin; Sporulation.
SQ SOURCE 719 AA; 81403 MW; F335F689D3B0C45 CRC64;

Query Match 9.8%; Score 325; DB 1; Length 719;
Best Local Similarity 22.5%; Pred. No. 2e-14;
Matches 145; Conservative 101; Mismatches 255; Indels 144; Gaps 27;

OY 52 PLVGVSSFLIKKVGSLIGKRLISLWGLIFPGSTNNMODILRETRQFLNRLNDTLA 111
DB 77 PPAQGVAS-----LVSFLIGELM-----PKGSKQ-WEIMEHVELINQKISTYAN 122
OY 112 RVNAELBGLQANTIRENQOVNFI-NFTQNPVPLSTSVNTMOQLFNLPRFGVQ 170
DB 123 KALADLKIGDALAVVHLESWMENNNRNVSVKQYALBELMVQGLPSFAVSGEE 182
OY 171 LILPLPQOANHHLSFIDVVLNADKGLSAALTFTYQNYKNTTYSNVCINTYQTA 230
DB 183 VLLPFIYAQAAHHLLILLDASIFCKEWSSEIEISTFYNRQSCQTEVDYCEWYWG 242
OY 231 ---FQGLN---TRLDMLFRTYFNLVVEYSIMSLEPKQSLVSSGANL---YASG 279
DB 243 LNRLEGTVNASWVRVY---QFRBDTLMVLDVALPSPYDRMRPIFTSAQLTREYIDA 299

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OY 280 SEP-QQTGSFTSDW-----PFL-----YSLFQVNSN-YVLNG 310
DB 300 IGVHNNASFATWTWNNNAPSPSTIEAAVVRNHLDFLEQVITYSLSSWSTQYMMN 359
OY 311 FSGARLTQFPNIGLPGTTTHALLARVNVSGVSSGDIAVGNQNFSGSTFELPLL 370
DB 360 WGGHKL--EFTTIGTLNIST-----QGSTINSINPVL 391
OY 371 PFRSMULSGSDRGCVVYT-----NQ--TESFSTGLRCGAFARQNSNY 416
DB 392 PFTSDVVRTESSLAGNLFLTPVANGVRVDFMKVTPHIA-----DNFY 438
OY 417 FPDYFRNISGVPLVRNEDLRPLHNYEIRNIESPSGPGSLARVNVHKNKNTYA- 475
DB 439 YPGY-----AGTGTQDSENLPEFTTGQPNYESISHLSHG--LISSHYKALVYSW 491
OY 476 VHENGTMIHLAPEDYGTISPIHATQV-----NNQTFISEKFGNQDSLRFQSN 529
DB 492 TRISA-----DRTN-TINDSITQIPVKAFLPSGASVVRGPGTGGDI-LQRTWT 541
OY 530 TARYTLRGNGN-----SYNLARVSSLSGNSITRTINGRVYASVNTTNDGVNDGA 584
DB 542 GTFGDIRVNIWPPAQRRLIRKASVTNLEFHTSINGALNQGNSATNMR-GEUDYX 600
OY 585 RLIDINMGVYASDNTNVLDIN-TRNSGTQELANITFTYPL 628
DB 601 ARRTVGTTPSPSSNAOSTFTTGANNPSLDNEVYIDRIEFVPEV 645

RESULT 12
C1ID BACTE STANDARD, PRT, 719 AA.
AC 045709;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Pesticidal crystal protein cryIIb (insecticidal) delta-endotoxin
DE CryII(b) (crystalline entomocidal protoxin) (81 kDa crystal protein).
GN CryIIB OR CryII(B) OR CRVY OR CRVY465.
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OK NCBI_TaxID=1436;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=BR465;
RX MEDLINE=95314293; PubMed=7793960;
RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;
RT "Distribution of cryII-type insecticidal protein genes in Bacillus
RT thuringiensis and cloning of cryII-type genes from Bacillus
RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.
RT entomocidus.", Microbiol. 61:2402-2407(1995).
RL Appl. Environ. Microbiol. 61:2402-2407(1995).
CC -I- FUNCTION: PROMOTES COLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF CERTAIN COLEOPTERAN AND LEPIDOPTERAN SPECIES.
CC ACTIVE ON PLUTELLA XYLSTELLA BUT NOT ON BOMBYX MORI.
CC -I- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORIULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -I- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -I- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
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CC -----
DR EMBL; U07642; AAA82114.1; -.
DR PIR; I40590; I40590.

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DR HSSE; P02965; 1C1Y.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; endotoxin_C.
 DR InterPro; IPR005639; endotoxin_N.
 DR Pfam; PF00555; endotoxin_1.
 DR Pfam; PF03944; endotoxin_C_1.
 DR Pfam; PF03945; endotoxin_N_1.
 DR Toxin; Sporulation.
 SQ SEQUENCE 719 AA; 81295 MW; E8210ABEA976888 CRC64;
 Query Match 9.4%; Score 310.5; DB 1; Length 719;
 Best Local Similarity 22.7%; Pred. No. 1.9e-13;
 Matches 153; Conservative 116; Mismatches 259; Indels 145; Gaps 34;
 27 EHSKDTIKEMMEKRTDLSLYVA-PIGVTSFLLKKGSLIGRIISLIMGLIPPSG 85
 47 EHSID---PVSASTIGTIGIAGKILGTVPAQASLX-SFILGELM---PKG 97
 86 STNIMODILRETEQFLNRLTDTLARVALESLQANIRENOQDNFLNTPVPLS 145
 98 KQ-QWEIFMEHVEEILNOKILTYARNKALSDRLGDMAYHESLESWEVENRNTARS 156
 146 IT-SVNTMOQLFLARLPORVQCYQLLPLFAQANMHSFIRDVNLADENGISAAT 204
 157 VAKNOYALFLMFVOKLSFVSGSEVPLPIAQAAMHLHLRLDASIFGKEMGLASE 216
 205 LRTYQNYLKNYTESNCTYQTA---FRGLNTRLHDM-LERTYMFANFEYSIMS 260
 217 ISTFYNQYERTRDYSDHCKIMVNTGLNLRGNKASWVRNQRKMTLWDLVAF 276
 261 LFKYQSLV---VSSGANL---YASGSGP-QQTSFSDMPFLYSLFVNSVYVANGSG 313
 277 --SDTLVPIKTSGLREYVYALIGTVHQAFASTTW---YNNAPSPFASTE 326
 314 AELTQTPNIGLPGTTTHALLA---ARVYSGG---VSSGIGANVQNGSGSTFLP 366
 327 AAVIRS-PLHDLERKVTYISLSRMSNTQYNNMGHRLSRPIGALNT--- 376
 367 PLTFPVRSLWDGSDRGVTVNMQTESF---ESTLGLRCGAFARAGNSYFP 418
 377 ---STQSSINTSINPTLQFTRSDVYRTESLAGLN--- 409
 419 DFTIRNISGV---LVARNEDLARPLHY---NEIRNIS--PSGTPG- 457
 410 -FLQPVNGVPRVDFHMKFPTLPIASDN---FYLGAGVGTQLQSENEIPETTSQP 464
 458 GLRAY-----MVSVNRKNTYA-VHENGTMHLAEDYGTSTSPHATV--- 503
 465 NYESYSHRLSHIGLISASHVKAIVYMTHSA-----DRTN-TIEPVSITQIPLYKA 515
 504 -NNQRTTIFSEKFG-NQGDLSRFGSNTTARLYLRNGN---SYNLVARYSLGNGSTI 556
 516 FULSSGAIVRGPGFTGDLK-RKNTGFGDIRVNLPPAPARVVRKRASTTDIOF 573
 557 RVTINGRYTASVNTTINDGVNDNGARFLDINMGVAVDNTNVLDTNV-TNNGTQ 615
 574 HHSINGKAINQGNFSAVMNR-GEIDLKTRRTIGFTTPPSFSDVOSTFTIGAMNNSGNE 632
 616 FELANIMFVPTNL 628
 633 VYIDRIEFVPEV 645
 RESULT 13
 C9CA_BACTO STANDARD; PRT; 1157 AA.
 AC Q45733;
 DT 30-MAY-2000 (rel. 39, Created)
 DT 30-MAY-2000 (rel. 39, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE Pesticidal crystal protein cry9Ca (insecticidal delta-endotoxin
 DE Cry1Xc(a)) (Crystalline entomocidal protoxin) (130 kDa crystal
 DE protein).

GN CRY9CA OR CRY1XC(A).
 OS Bacillus thuringiensis (subsp. tolworthi).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OK NCBI_TaxId=1442;
 RN [1]
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
 RX STRAIN=B7502618A;
 RX MEDLINE=96141404; PubMed=8572715;
 RA Lambert B., Buysse L., Decock C., Jansens S., Plens C., Saey B.,
 RA Seurinck J., Van Audenhove K., Van Rie J., Van Vleet A., Refocon M.;
 RT "A Bacillus thuringiensis insecticidal crystal protein with a high
 RT activity against members of the family Noctuidae";
 RL Appl. Microbiol. 62:80-86(1996)
 CC -1- FUNCTION: PROMOTES COLPODOSPOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF LEPIDOPTERA LARVAE. HAS A FAIRLY BROAD
 CC SPECTRUM OF ACTIVITY AGAINST MEMBERS OF THE FAMILIES PYRALIDAE,
 CC PLUTELIDAE, SPHINGIDAE, AND NOCTUIDAE. IT IS THE FIRST
 CC INSECTICIDAL CRYSTAL PROTEIN WITH ACTIVITY AGAINST CUTWORMS. NO
 CC ACTIVITY IS OBSERVED AGAINST SOME BEETLES, SUCH AS COLORADO POTATO
 CC BEETLE.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF
 CC THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-
 CC TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; Z37527; CAA85764.1; -;
 CC PIR; A59350; 849247.
 DR HSSE; P07130; 1DLC.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; endotoxin_C.
 DR InterPro; IPR005639; endotoxin_N.
 DR Pfam; PF00555; endotoxin_1.
 DR Pfam; PF03944; endotoxin_C_1.
 DR Pfam; PF03945; endotoxin_N_1.
 DR Toxin; Sporulation.
 SQ SEQUENCE 1157 AA; 129775 MW; C364391EF7FDB8A CRC64;
 Query Match 9.3%; Score 307; DB 1; Length 1157;
 Best Local Similarity 23.4%; Pred. No. 6.4e-13; Indels 232; Gaps 34;
 Matches 163; Conservative 87; Mismatches 215;
 52 PIVGVTSFLLKKGSLIGRIISLIMGLIPPSGTVNLMODILRETEQFLNRLTDTLA 111
 87 PFGQIVSYF---QFLNTLM---PVNDTAWFAERQVEELVNOQTTERARN 133
 112 RVNALESLQANIRENOQDNFL---NPTONPVPLSITSVNTMOQ-FLNTRPQFRVQ 167
 134 QALARQLGDSENVYQSLQNLMDLRDNRV---LSVRAQFIALDDPNAALPLEFANV 190
 168 GYQLLPLFAQANMHSFIRDVNLADENGISAATLRTYQNYLKNYTESNCTYQ 227
 191 GQGVPLSYVAQAVNLHLKLDASIFGEGWPGTGISISYVROLELTARTYVCTWY 250
 228 QTA---FRGLNTR---RLHDMLEFRTYMFANFEYSIMSFLFYQSLVYSSGANLYVSSG 280
 251 NTGLDRKNTESWLKH---QPRKMTLVLDV---ALFPYVYV---RLYPTGS 298
 281 GPQQTQS-FTS-----QDM-----PFLY-----S 298
 299 NQQLTREVTDTIVENPPANVGLCRMGTNPYNTFSELENAFIRPHLFDRLNSITSSN 358
 299 LFOVNSVYVNLNFGSARLQTFPNIQGLG-----TTTHALLARVNSGGVSGDIG- 352

Db 359 REPVSNNF-MDYSGHTLRSLYNDASVOEDSYGLITTTTPRATNPVGDTNRISTAVDF 417
 QY 353 -----AVFNONFSCSTFLPLLPFFVRSWTDGSD---RGAVNV---TNMGQESFESTLG 402
 Db 418 RSALIGIYGN-----RASFPVGGIENKTTSPANGCGRUYTHNDELPDEST-- 465
 QY 403 LRCAAFARAGNSNYPEDY-----FINNISGVLV---ENEDLRPLHNEIRNIESPS 453
 Db 466 ---GSSYTHRSHTVFFSFTQNAQASINAGSVPTVYWRDVLNNTIPNRILOLP--- 519
 QY 454 GTPGGLRAYVSVHNRKNNIYAHENGTMTIHLAPEDYGFETSPHATQVNNQOTFTISE 513
 Db 520 -----LVKA-----SAPVSTYTLAKP-----GTF----- 539
 QY 514 KFGNGDSLAFEGSNTTARYTLRGNNS-----YMLYRVSLSLGNSTIRVTIN---GRV 564
 Db 540 ---GGGILKRTTNGTFG---TLRYTVNSPLTQYRLRVAFSTNPFISIVLKGVSIDV 593
 QY 565 YTAGNVN-----TTT-----NNDGVNDNGARPLD--- 588
 Db 594 RLGSYMRGQELTFYESFTFRFTTTGPFNPFTFPGQAEILLTVNABGVSTGGERYIIDRIE 653
 QY 589 ---INMGVNVASD-----NTNVPLDINVT 609
 Db 654 IVPNPARAEEDLEAKKAVASLFTETRDGLQVNTT 690

RESULT 14
 ID C7AB BACUA STANDARD; PRT; 1138 AA.
 AC 045707:
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pesticidal crystal protein cry7ab (insecticidal delta-endotoxin
 CryVIIa(b) (Crystalline entomocidal protoxin) (139 kDa crystal
 protein).
 GN CRY7AB OR CRYVIIA(B).
 OS Bacillus thuringiensis (subsp. dakota).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=132268;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=HD511;
 RA Payne J.M., Fu J.M.;
 RT "Coleopteran-active toxins";
 RT coleopteran-active toxins";
 RL Patent number US5286486, 15-FEB-1994.
 CC -1- FUNCTION: PROMOTES COLICIDIOSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF COLEOPTERA.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF
 CC THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-
 CC TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
 CC
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 CC
 CC EMBL; 004367; AAA21120.1; .
 DR HSSP; P07130; IDLC.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; endotoxin_C.
 DR InterPro; IPR005639; endotoxin_N.
 DR Pfam; PF00555; endotoxin_1.
 DR Pfam; PF03944; endotoxin_C_1.
 DR Pfam; PF03945; endotoxin_N_1.

KM Toxin: Sporulation.
 SQ SEQUENCE 1138 AA; 129778 MW; 01DF7072C074CE88 CRC64;
 Query Match 9.2%; Score 306; DB 1; Length 1138;
 Best Local Similarity 20.0%; Pred. No. 7.3e-13;
 Matches 135; Conservative 109; Mismatches 22; Indels 208; Gaps 25;

QY 52 PIVGVSSFLKKVQSLIGRIILSELMLIPFGSGTYLMODILRETEGLOMORTNTDTLA 111
 Db 76 FGASFITNLYK-----ITGLWPH-NKXIMBERTEVETLIDKLEQVARN 121
 QY 112 RVNAHEEGIANIRFNOQVDNFTLPQNPVLS-ITSSVNTMOQLFNRLPQRFVQYQ 170
 Db 122 KALAELEGANNLTITYOALDELDNPDPAITIRVIDREFRIDALFESVMPSEFVAGYE 181
 QY 171 LLLPLPFAQANMHLSPFRDVNLNADWEGISATLFTYQNYLKNVYTESNYCINTQTA 230
 Db 182 IPLLTVYAQANLHLALRDLSTLYGDKGFTQNNIENNRQKKHISESHNCVKWNSG 241
 QY 231 FRGLNRLHDL---ERTYPLAVFEVYSIWSLFKYQSLVSSGANLVASGSGPOQTQ 286
 Db 242 LSRINGSTYEQMINVNRFRKMTLWDLAIVFYD----- 278
 QY 287 SFTSQDMPFLYSLEQVANSNYVLNGFSGARLTQTFPNIGLPGTTTHALLAARVSGCV 346
 Db 279 -----PRMSW-----ET-----STQLREVYTDISTLS-I 303
 QY 347 SSGDIGAVNQNFCSTFLPLLPFFVRSWTD----- 378
 Db 304 SNPDIGPFSQWEMNTA-----FRTPHLDVYIDELIYTSKYAFSHEIOPDLFWCVKHY 358
 QY 379 ---SGSDRGVNTVYNNQTESFEFTLG-LRCGAFARAGNSNYPEDYFINISGVLVRNE 435
 Db 359 SFKSSQSNVLT---TGAYGTSGYISGAYSFRENDIY---RTLAAPVVV--- 404
 QY 436 DLRPLHNEIRNIES-GRFGGLRAYVSVHNRKNNIY-----AVHE 478
 Db 405 ---YPTQYGVGEQVEFYGVNG---HAYRGDNKTYDLYDSIDQLPPDGEIHE 452
 QY 479 -----NGTMIHLAPEDYGFETSPHATQVNNQOTFTISEFQNGDSLRFQSVNTTA 531
 Db 453 KYTHRLCHNTAISKSTPDYDNATL-PIFSW-----THRSAYNRYLPKIKKIPAVK 504
 QY 532 RYTL-----RG-NG-----NSNYLRLRSSLSNSTIR 557
 Db 505 MYGLDLSLVYKGGFTGSDLVKRGSGNYIDIRATVNSPLQKTRVRYATVSGLFN 564
 QY 558 VTINGRVYTAASNVNTT---TNNDGVNDNGARPLDINMGVNASDNTNVPLDINVT-FNSGT 614
 Db 565 VFINDIELAQNNFQSVTETIGEGKDLVYGSFYIEVSTTIQFPNHPKLTILHNLHNSNS 624
 QY 615 QFELNIMVEFPTN 628
 Db 625 PFTVDSIEPIFVDV 638

RESULT 15
 ID C1BE BACTU STANDARD; PRT; 1227 AA.
 AC 085805:
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Pesticidal crystal protein cryIbE (insecticidal delta-endotoxin
 CryIbE) (Crystalline entomocidal protoxin) (139 kDa crystal protein).
 GN CRYIbE OR CRYIb(E) OR I58C2B.
 OS Bacillus thuringiensis.
 OG Plasmid pMV2383.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL B-18872 / PS158C2;

RA Payne J.M., Cummings D.A., Cannon R.J.C., Narva K.E., Srelnan S.;
 RT "Bacillus thuringiensis genes encoding lepidopteran-active toxins."
 RL Patent number US5723758, 03-MAR-1998.
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPORE germination AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
 CC -----
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 CC -----
 CC DR EMBL; AF077326; AAC32850.1; -.
 CC DR HSSP; P07130; 1DLC.
 CC DR Interpro; IPR001178; Endotoxin.
 CC DR Interpro; IPR005639; endotoxin_C.
 CC DR Interpro; IPR005639; endotoxin_N.
 CC DR Pfam; PF00555; endotoxin_1.
 CC DR Pfam; PF03944; endotoxin_C_1.
 CC DR Pfam; PF03945; endotoxin_N_1.
 CC DR Toxin; Sporulation; Plasmid.
 CC KW SEQUENCE 1227 AA; 139084 MW; CBA847BEA0B34CD3 CRC64;
 SQ
 - Query Match 9.2%; Score 305.5; DB 1; Length 1227;
 Best Local Similarity 22.5%; Pred. No. 8.8e-13;
 Matches 142; Conservative 101; Mismatches 265; Indels 123; Gaps 25;
 QY 52 PLVGVSSFLKKGSLGKRLISLNGLIFFSGSTNLMODLRTQFLNQLNTDTLA 111
 DB 73 PFAGQIASFFSYFLVG-----ELW---PRG-RDPWEIPLHEVEQLIRQOVTEITRD 118
 QY 112 RVNAELGEGIANIREFNOVDNPLNPTQNPVPLSITTSVNTMOQL-PLNRLPQFRVQGYQ 170
 DB 119 TLAARLQGLGNSPFAVQGLSLEDLNRDARTSVLYTQYIALDELPLNMPLEAIRNQE 178
 QY 171 LLLPLPFAQANNAHLSTIRPVLANDEWGISATLRTQNYLAKYTTESNYCINTYQA 230
 DB 179 VPLWVYAQAANLHLTLRLDASLPSEBGLTSQETIQRYEROVETKREISDYCARWYNTG 238
 QY 231 FRGL-NTRLADML---EFTYMLNVFVYSIMSLFKYOSLIVSSGANTL---YASGSGP 282
 DB 239 LNNLAGTNAESMLKRYNQFRDLTLGLDLVALPSPYDTRVYPMNTSAQLTREIYTDPIGR 298
 QY 283 QQTQS-FTSQDPFLVSLPQVNSNYVINGSGARLTQTF-PNIGLPGTTTHALLAARV 340
 DB 299 TNAISGFASTW-----FNNN-APSFSAIEAAVIRPPLDLPPEQLTIFSVLSRWS 348
 QY 341 NTSGVSSGDIGAVNQNFSCSTFLPPLLPFVHSW-----LDGSDRGVNVYTN----- 391
 DB 349 N-----TOYMYWVGRLSRTIRGSLSTSHGNTNT 380
 QY 392 -----WQTESPES-----TLGARGCAPTARGSNYPDPYFIANI--SG 427
 DB 381 SINPVTLQFTSRDYRTSPAGINILITTPVNGVPMARFWKRPILNSLRGSLYTYGTYG 440
 QY 428 VPLVYRNEDLRPLHYNEIRNIESPGPGGLRAYVSVNKRNNIYA-VHENGTMHLA 486
 DB 441 VGTQLPDSBELPEETERPNYESYHRLSNIR--LISGNTLAPVYSWTHRSA----- 492
 QY 487 PEDYGFITSPHATON-----NQRTFISKEFGNODSLRFEOSNTTARTYLRKNG 539
 DB 493 --DRIN-TISSDSITQIPLYKSPNLSGTSVSGPGTGDIIKTNVGSVLSMGANFNN 549
 QY 540 NS---YNLYRVSSLSGSTRVING-RVYTASNVTNTTNDGVNDGAPPLDINMGVNV 595

DB 550 TSLQRYRVRYRYAASQWLVRLTVYGGSTTFDQGFPSITMSANESLTSQSGFRPAEPVGISA 609

QY 596 ASDNTVPIPDIVTNSGTO-FELNIMFVP 625

DB 610 SGSGT--AGISISNNAGROTFFHDKLFIIP 637

Search completed: August 14, 2003, 18:11:19
 Job time : 17 sec

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OM protein - protein search, using SW model

Run on: August 14, 2003, 18:08:52 ; Search time 46 Seconds

(without alignments)
3545.418 Million cell updates/sec

Title: US-10-040-906A-2

Sequence: 1 MNVNLNGRTTICDANYVVA.....GTQELNIMFVPTNLPPIY 632

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_RMBL_23:*
2: SP_Bacteria:*
3: SP_Fungi:*
4: SP_Human:*
5: SP_Invertebrate:*
6: SP_Mammal:*
7: SP_mhc:*
8: SP_Organelle:*
9: SP_Phage:*
10: SP_Plant:*
11: SP_Rodent:*
12: SP_Virus:*
13: SP_Vertebrate:*
14: SP_Unclassified:*
15: SP_Virus:*
16: SP_Bacteriap:*
17: SP_Archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3044.5	91.9	633	2 Q8GHR3	Q8GHR3 bacillus ch
2	3029.5	91.4	633	2 Q9S6N5	Q9S6N5 bacillus ch
3	3025.5	91.3	633	2 Q9S6N4	Q9S6N4 bacillus ch
4	2998.5	90.5	633	2 Q8GHR0	Q8GHR0 bacillus ch
5	2641.5	79.7	551	2 Q8RM99	Q8RM99 bacillus ch
6	328.5	9.9	1231	2 Q8KNY2	Q8KNY2 bacillus ch
7	327.5	9.9	719	2 Q9JNT5	Q9JNT5 bacillus ch
8	325.5	9.8	719	2 Q8J796	Q8J796 bacillus ch
9	323.5	9.8	719	2 Q8K161	Q8K161 bacillus ch
10	317.5	9.6	719	2 Q9F0P8	Q9F0P8 bacillus ch
11	280.5	8.5	1180	2 Q9S5Y8	Q9S5Y8 bacillus ch
12	279.5	8.4	645	2 Q9S603	Q9S603 bacillus ch
13	278.5	8.4	1228	2 Q9JNMS	Q9JNMS bacillus ch
14	276.5	8.3	381	2 Q45740	Q45740 bacillus ch
15	276.5	8.3	620	2 Q45720	Q45720 bacillus ch
16	276.5	8.3	1176	2 Q45736	Q45736 bacillus ch

17	276.5	8.3	1228	2 Q9J775	Q9J775 bacillus ch
18	274.5	8.2	1176	2 Q9S514	Q9S514 bacillus ch
19	270.5	8.2	1176	2 Q9AM83	Q9AM83 bacillus ch
20	270.5	8.2	1176	2 Q9RC30	Q9RC30 bacillus ch
21	270.5	8.1	1177	2 Q8GLY5	Q8GLY5 bacillus ch
22	268	8.1	1155	2 Q9F296	Q9F296 bacillus ch
23	264.5	8.0	1178	2 Q9R826	Q9R826 bacillus ch
24	264	8.0	723	2 Q9S4B5	Q9S4B5 bacillus ch
25	264	8.0	1174	2 Q45749	Q45749 bacillus ch
26	264	8.0	1177	2 Q03743	Q03743 bacillus ch
27	263	7.9	1155	2 Q9J721	Q9J721 bacillus ch
28	262.5	7.9	1144	2 Q8K2L7	Q8K2L7 bacillus ch
29	262	7.9	638	2 Q87654	Q87654 bacillus ch
30	261.5	7.9	1178	2 Q45768	Q45768 bacillus ch
31	259	7.8	1177	2 Q45735	Q45735 bacillus ch
32	257.5	7.8	1236	2 Q939T3	Q939T3 bacillus ch
33	255.5	7.7	618	2 Q32306	Q32306 bacillus ch
34	255	7.7	1118	2 Q9AM82	Q9AM82 bacillus ch
35	253	7.6	607	2 Q45721	Q45721 bacillus ch
36	253	7.6	618	2 Q45737	Q45737 bacillus ch
37	250	7.5	652	2 Q9S6N9	Q9S6N9 bacillus ch
38	246	7.4	1169	2 Q8GHE8	Q8GHE8 bacillus ch
39	244	7.4	1160	2 Q93TF9	Q93TF9 bacillus ch
40	237	7.2	650	2 Q8VNX2	Q8VNX2 bacillus ch
41	231.5	7.0	1189	2 Q9L877	Q9L877 bacillus ch
42	230	6.9	660	2 Q8ROU6	Q8ROU6 bacillus ch
43	216	6.5	1144	2 Q45745	Q45745 bacillus ch
44	214.5	6.5	1171	2 Q06894	Q06894 bacillus ch
45	212	6.4	723	2 Q9EVR2	Q9EVR2 bacillus ch

ALIGNMENTS

RESULT 1

Q8GHR3 PRELIMINARY: PRT; 633 AA.
ID Q8GHR3
AC Q8GHR3; 01-MAR-2003 (TREMURel. 23, Created)
DT 01-MAR-2003 (TREMURel. 23, Last sequence update)
RT 01-MAR-2003 (TREMURel. 23, Last annotation update)
DE Insecticidal crystal protein Cry2A.
CN CRY2A.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OK NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Dongbei 66;
RA Wei G., Jie Z., Dafang H., Guoxun L.;
RT "New cry2A gene from Chinese native isolates Bt strain Dongbei 66,"
RL Submitted (ABR-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF252622; NC013734.1; -
SQ SEQUENCE 633 AA; 70822 MW; 9CA1999187898A6 CRC64;

Query Match 91.9%; Score 3044.5; DB 2; Length 633;
Best local Similarity 90.5%; Pred. No. 1e-196;
Matches 573; Conservative 34; Mismatches 25; Indels 1; Gaps 1;

Qy	1	MNVNLNGRTTICDANYVVAADPFSEHSLTTRKEMWERTDHSIYVAVGVSSSF	60
Db	1	MNVNLNGRTTICDANYVVAADPFSEHSLTTRKEMWERTDHSIYVAVGVSSSF	60
Qy	61	LKKVGLSGKRIILSELWGLIFPSGSTNIMODILRETOFANORLNTDTLAVNAEGL	120
Db	61	LKKVGLSGKRIILSELWGLIFPSGSTNIMODILRETOFANORLNTDTLAVNAEGL	120
Qy	121	QANIRENOVDNFPNPNVPELSTSSVNTMOQLFLANLPFRVGYQLLLPLFAQA	180
Db	121	QANIRENOVDNFPNPNVPELSTSSVNTMOQLFLANLPFRVGYQLLLPLFAQA	180
Qy	181	ANWHSFIRDVVLANDEWGISAAITRTYQNIKMYTTEYSNICYQTAFGLNTRLHD	240
Db	181	ANWHSFIRDVVLANDEWGISAAITRTYQNIKMYTTEYSNICYQTAFGLNTRLHD	240


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Db 181 ANHLSFIRIDVILNADENWISAAATLRTYDYLAHYTRDYSNVCINTYOTAFRGLNTRLHD 240
Qy 241 MLEFRTYFLNFEVYSIWSLFFKQSLVSSGANLYASGSGPOQTOSFTSQDMPFLYSLE 300
Db 241 MLEFRTYFLNFEVYSIWSLFFKQSLVSSGANLYASGSGPOQTOSFTSQDMPFLYSLE 300
Qy 301 QVNSNYVLNGFSGALRTOTFPNIGGLPGTTTHALLAARVNSGVSSGSDIGAV-FNOME 359
Db 301 QVNSNYVLNGFSGALRTOTFPNIGGLPGTTTHALLAARVNSGVSSGSDIGAV-FNOME 360
Qy 360 SCSTFLPPLLPFRVMSLDSGDRGVNTVMQTESFESTLRCGAPFARGNSYFPD 419
Db 361 NCSTVLPPLSTPFRVMSLDSGDRGVNTVMQTESFESTLRCGAPFARGNSYFPD 420
Qy 420 YFIRNISGVPLVVRNEDLRPLAHNEIRNIESPSGTPGGLRAYVNSVHNRKNNTYAVHEN 479
Db 421 YFIRNISGVPLVVRNEDLRPLAHNEIRNIESPSGTPGGLRAYVNSVHNRKNNTYAVHEN 480
Qy 480 GTMTHLAPEDYTGFTISPIHATOVNNQRTFISEKFGNODSLRFGOSNTTARATLARGNG 539
Db 481 GTMTHLAPEDYTGFTISPIHATOVNNQRTFISEKFGNODSLRFGOSNTTARATLARGNG 540
Qy 540 NSYNLYLWSSLGNSSTIRVINGRVYTAASVNTTNDGVNDGARFLDINMGVYASDN 599
Db 541 NSYNLYLWSSLGNSSTIRVINGRVYTAASVNTTNDGVNDGARFLDINMGVYASDN 600
Qy 600 TNPVLDINTVNSGTOFELNIMFVPTNLPPIY 632
Db 601 TNPVLDINTVNSGTOFELNIMFVPTNLPPIY 633

```

RESULT 2

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09S6N5 PRELIMINARY; PRT; 633 AA.
ID 09S6N5
AC 09S6N5:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE cry2Aa protein.
GN cry2Aa.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=Y271;
RA Yu J., Pang Y.;
RT "Cloning and characterisation of insecticidal crystal protein gene
RT cry2Aa from new isolated strain of Bacillus thuringiensis Y271.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ132465; CAA10672.1; -
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
SQ SEQUENCE 633 AA; 70837 MW; CC727E33B75A583 CRC64;

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Query Match 91.4%; Score 3029.5; DB 2; Length 633;

Best Local Similarity 90.0%; Pred. No. 1.1e-195;

Matches 570; Conservative 36; Mismatches 26; Indels 1; Gaps 1;

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Qy 1 MNVNLNGRTTICDAVNVVAHDPSPFEHKSLDITRKEMEMKRTDHSLYVAPVGVTSF 60
Db 1 MNVNLNGRTTICDAVNVVAHDPSPFEHKSLDITRKEMEMKRTDHSLYVAPVGVTSF 60
Qy 61 LKKGVSLLIGKRIISLSELMGLIFPSGSTNLMODILRETEQFLNQRLNTDTLARVNAELGL 120
Db 61 LKKGVSLLIGKRIISLSELMGLIFPSGSTNLMODILRETEQFLNQRLNTDTLARVNAELGL 120
Qy 121 QANIREFNOQVDNPLNPTONPVPLSTSSVNTMOQLFLNLRPFQFQIGYOLLPLPFAQA 180
Db 121 QANIREFNOQVDNPLNPTONPVPLSTSSVNTMOQLFLNLRPFQFQIGYOLLPLPFAQA 180

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Qy 181 ANHLSFIRIDVILNADENWISAAATLRTYDYLAHYTRDYSNVCINTYOTAFRGLNTRLHD 240
Db 181 ANHLSFIRIDVILNADENWISAAATLRTYDYLAHYTRDYSNVCINTYOTAFRGLNTRLHD 240
Qy 241 MLEFRTYFLNFEVYSIWSLFFKQSLVSSGANLYASGSGPOQTOSFTSQDMPFLYSLE 300
Db 241 MLEFRTYFLNFEVYSIWSLFFKQSLVSSGANLYASGSGPOQTOSFTSQDMPFLYSLE 300
Qy 301 QVNSNYVLNGFSGALRTOTFPNIGGLPGTTTHALLAARVNSGVSSGSDIGAV-FNOME 359
Db 301 QVNSNYVLNGFSGALRTOTFPNIGGLPGTTTHALLAARVNSGVSSGSDIGAV-FNOME 360
Qy 360 SCSTFLPPLLPFRVMSLDSGDRGVNTVMQTESFESTLRCGAPFARGNSYFPD 419
Db 361 NCSTVLPPLSTPFRVMSLDSGDRGVNTVMQTESFESTLRCGAPFARGNSYFPD 420
Qy 420 YFIRNISGVPLVVRNEDLRPLAHNEIRNIESPSGTPGGLRAYVNSVHNRKNNTYAVHEN 479
Db 421 YFIRNISGVPLVVRNEDLRPLAHNEIRNIESPSGTPGGLRAYVNSVHNRKNNTYAVHEN 480
Qy 480 GTMTHLAPEDYTGFTISPIHATOVNNQRTFISEKFGNODSLRFGOSNTTARATLARGNG 539
Db 481 GTMTHLAPEDYTGFTISPIHATOVNNQRTFISEKFGNODSLRFGOSNTTARATLARGNG 540
Qy 540 NSYNLYLWSSLGNSSTIRVINGRVYTAASVNTTNDGVNDGARFLDINMGVYASDN 599
Db 541 NSYNLYLWSSLGNSSTIRVINGRVYTAASVNTTNDGVNDGARFLDINMGVYASDN 600
Qy 600 TNPVLDINTVNSGTOFELNIMFVPTNLPPIY 632
Db 601 TNPVLDINTVNSGTOFELNIMFVPTNLPPIY 633

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RESULT 3

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09S6N4 PRELIMINARY; PRT; 633 AA.
ID 09S6N4
AC 09S6N4:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE cry2Aa protein.
GN cry2Aa.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=SL39;
RA Yu J., Pang Y.;
RT "Cloning and characterisation of insecticidal crystal protein gene
RT cry2Aa from new isolated strain of Bacillus thuringiensis SL39.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ132464; CAA10671.1; -
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
SQ SEQUENCE 633 AA; 70925 MW; 8FB7F5216AC6F7B8 CRC64;

```

Query Match 91.3%; Score 3025.5; DB 2; Length 633;

Best Local Similarity 90.0%; Pred. No. 2e-195;

Matches 570; Conservative 35; Mismatches 27; Indels 1; Gaps 1;

```

Qy 1 MNVNLNGRTTICDAVNVVAHDPSPFEHKSLDITRKEMEMKRTDHSLYVAPVGVTSF 60
Db 1 MNVNLNGRTTICDAVNVVAHDPSPFEHKSLDITRKEMEMKRTDHSLYVAPVGVTSF 60
Qy 61 LKKGVSLLIGKRIISLSELMGLIFPSGSTNLMODILRETEQFLNQRLNTDTLARVNAELGL 120
Db 61 LKKGVSLLIGKRIISLSELMGLIFPSGSTNLMODILRETEQFLNQRLNTDTLARVNAELGL 120
Qy 121 QANIREFNOQVDNPLNPTONPVPLSTSSVNTMOQLFLNLRPFQFQIGYOLLPLPFAQA 180
Db 121 QANIREFNOQVDNPLNPTONPVPLSTSSVNTMOQLFLNLRPFQFQIGYOLLPLPFAQA 180

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Db      121 QANIREFOVDNFANPTONPVPLSTSSVNTMOQLFLNRLPFOIOGYOLLPLPFAQA 180
Qy      181 AMHLSFTRDVVNLNADENWGISAAATLRTYQVNLKNTYTESYNCINTYQTAFRGLNTRLHD 240
Db      181 AMHLSFTRDVVNLNADENWGISAAATLRTYQVNLKNTYTESYNCINTYQTAFRGLNTRLHD 240
Qy      241 MLEPRTYMLNFEYYSIWSLFKXOSILVSSGANLYASGGPOQOTSFISQDMPPLYSLF 300
Db      241 MLEPRTYMLNFEYYSIWSLFKXOSILVSSGANLYASGGPOQOTSFISQDMPPLYSLF 300
Qy      301 QVNSNYVLNFGSGARLTOTFPNIGLPGTTTHALLAARVNVSGVSSGDIAGV-FQNGF 359
Db      301 QVNSNYVLNFGSGARLTOTFPNIGLPGTTTHALLAARVNVSGVSSGDIAGV-FQNGF 359
Qy      360 SCSTFPLPLLPFVPSWLDGSDRGVNTVMQTESFEESTLGLRCGAFARGSNFYPPD 419
Db      360 SCSTFPLPLLPFVPSWLDGSDRGVNTVMQTESFEESTLGLRCGAFARGSNFYPPD 419
Qy      361 NCSTFPLPLLPFVPSWLDGSDRGVNTVMQTESFEESTLGLRCGAFARGSNFYPPD 420
Db      361 NCSTFPLPLLPFVPSWLDGSDRGVNTVMQTESFEESTLGLRCGAFARGSNFYPPD 420
Qy      420 YFIRNLSGVLVVRNEDLRPLHYNELRNIESPSGPGGLRAVYVSHNRKNNTYAVHEN 479
Db      420 YFIRNLSGVLVVRNEDLRPLHYNELRNIESPSGPGGLRAVYVSHNRKNNTYAVHEN 479
Qy      480 GTMHLAPEDYTGFTISPIHATOVNNOQRTFISEKFGQSDSLRFEQSNNTARYTLRANG 539
Db      480 GTMHLAPEDYTGFTISPIHATOVNNOQRTFISEKFGQSDSLRFEQSNNTARYTLRANG 539
Qy      481 GTMHLAPEDYTGFTISPIHATOVNNOQRTFISEKFGQSDSLRFEQSNNTARYTLRANG 540
Db      481 GTMHLAPEDYTGFTISPIHATOVNNOQRTFISEKFGQSDSLRFEQSNNTARYTLRANG 540
Qy      540 NSYMLYLRVSSLGSTIRVTINGRVYTAASVNTTNDGVNDGARFLDIMGVNASDN 599
Db      541 NSYMLYLRVSSLGSTIRVTINGRVYTAASVNTTNDGVNDGARFLDIMGVNASDN 599
Qy      600 TNPVLDINTVNSGTOPELMNIMFVPTNLPRY 632
Db      601 TNPVLDINTVNSGTOPELMNIMFVPTNLPRY 633

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RESULT 4

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ID      08GH90      PRELIMINARY;      PRT;      633 AA.
AC      08GH90;
DT      01-MAR-2003 (T-EMBLrel. 23, Created)
DT      01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT      01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
GN      Crystal delta-endotoxin.
OS      Bacillus thuringiensis.
OC      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX      NCBI_TaxID=1428;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=B-pr-88;
RA      Li C., Zhang J., Huang D., Li G.;
RT      "A crystal endotoxin from Bacillus thuringiensis strain B-pr-88."
RL      Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF361115; AAO13296.1;
SQ      SEQUENCE 633 AA; 70726 MW; 01EFA3A35564D01 CRC64;

```

Query Match 90.5%; Score 2998.5; DB 2; Length 633;
 Best Local Similarity 89.4%; Pred. No. 1.3e-193;
 Matches 566; Conservative 40; Mismatches 26; Indels 1; Gaps 1;

```

Qy      1 MNNVNLNGRTTICDAYNVVAHDPFSFEHKSIDTIRKEMWEMKRTDHSLYVAVPTGVSSF 60
Db      1 MNNVNLNGRTTICDAYNVVAHDPFSFEHKSIDTIRKEMWEMKRTDHSLYVAVPTGVSSF 60
Qy      61 LKLVGSLIGKRILSELWGLIFPSGSTNLMODILRETEQFLNORLNTDYLARVNAELRGL 120
Db      61 LKLVGSLIGKRILSELWGLIFPSGSTNLMODILRETEQFLNORLNTDYLARVNAELRGL 120
Qy      121 QANIREFOVDNFANPTONPVPLSTSSVNTMOQLFLNRLPFOIOGYOLLPLPFAQA 180
Db      121 QANIREFOVDNFANPTONPVPLSTSSVNTMOQLFLNRLPFOIOGYOLLPLPFAQA 180
Qy      181 AMHLSFTRDVVNLNADENWGISAAATLRTYQVNLKNTYTESYNCINTYQTAFRGLNTRLHD 240

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Db      181 AMHLSFTRDVVNLNADENWGISAAATLRTYQVNLKNTYTESYNCINTYQTAFRGLNTRLHD 240
Qy      241 MLEPRTYMLNFEYYSIWSLFKXOSILVSSGANLYASGGPOQOTSFISQDMPPLYSLF 300
Db      241 MLEPRTYMLNFEYYSIWSLFKXOSILVSSGANLYASGGPOQOTSFISQDMPPLYSLF 300
Qy      301 QVNSNYVLNFGSGARLTOTFPNIGLPGTTTHALLAARVNVSGVSSGDIAGV-VERQNF 359
Db      301 QVNSNYVLNFGSGARLTOTFPNIGLPGTTTHALLAARVNVSGVSSGDIAGV-VERQNF 359
Qy      360 SCSTFPLPLLPFVPSWLDGSDRGVNTVMQTESFEESTLGLRCGAFARGSNFYPPD 419
Db      360 SCSTFPLPLLPFVPSWLDGSDRGVNTVMQTESFEESTLGLRCGAFARGSNFYPPD 419
Qy      361 NCSTFPLPLLPFVPSWLDGSDRGVNTVMQTESFEESTLGLRCGAFARGSNFYPPD 420
Db      361 NCSTFPLPLLPFVPSWLDGSDRGVNTVMQTESFEESTLGLRCGAFARGSNFYPPD 420
Qy      420 YFIRNLSGVLVVRNEDLRPLHYNELRNIESPSGPGGLRAVYVSHNRKNNTYAVHEN 479
Db      420 YFIRNLSGVLVVRNEDLRPLHYNELRNIESPSGPGGLRAVYVSHNRKNNTYAVHEN 479
Qy      480 GTMHLAPEDYTGFTISPIHATOVNNOQRTFISEKFGQSDSLRFEQSNNTARYTLRANG 539
Db      480 GTMHLAPEDYTGFTISPIHATOVNNOQRTFISEKFGQSDSLRFEQSNNTARYTLRANG 539
Qy      481 GSHMLAPEDYTGFTISPIHATOVNNOQRTFISEKFGQSDSLRFEQSNNTARYTLRANG 540
Db      481 GSHMLAPEDYTGFTISPIHATOVNNOQRTFISEKFGQSDSLRFEQSNNTARYTLRANG 540
Qy      540 NSYMLYLRVSSLGSTIRVTINGRVYTAASVNTTNDGVNDGARFLDIMGVNASDN 599
Db      541 NSYMLYLRVSSLGSTIRVTINGRVYTAASVNTTNDGVNDGARFLDIMGVNASDN 599
Qy      600 TNPVLDINTVNSGTOPELMNIMFVPTNLPRY 632
Db      601 SDVPLDINTVNSGTOPELMNIMFVPTNLPRY 633

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RESULT 5

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ID      09RM89      PRELIMINARY;      PRT;      551 AA.
AC      09RM89;
DT      01-MAY-2000 (T-EMBLrel. 13, Created)
DT      01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT      01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE      Cry2A protein (Fragment).
GN      CRY2AD.
OS      Bacillus thuringiensis.
OC      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX      NCBI_TaxID=1428;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Cy29;
RA      Yu J., Pang Y.;
RT      "Cloning and characterization of insecticidal crystal protein gene
RL      cry2Ad from new isolated strain of Bacillus thuringiensis Cy29."
DR      EMBL; AJ132463; CAA10670.2;
DR      InterPro; IPR005639; endotoxin_N.
DR      Pfam; PF03945; endotoxin_N.1.
FT      NON_TER 551
SQ      SEQUENCE 551 AA; 62126 MW; D6B778A8E713B98A CRC64;

```

Query Match 79.7%; Score 2641.5; DB 2; Length 551;
 Best Local Similarity 90.4%; Pred. No. 1.2e-169;
 Matches 498; Conservative 30; Mismatches 22; Indels 1; Gaps 1;

```

Qy      1 MNNVNLNGRTTICDAYNVVAHDPFSFEHKSIDTIRKEMWEMKRTDHSLYVAVPTGVSSF 60
Db      1 MNNVNLNGRTTICDAYNVVAHDPFSFEHKSIDTIRKEMWEMKRTDHSLYVAVPTGVSSF 60
Qy      61 LKLVGSLIGKRILSELWGLIFPSGSTNLMODILRETEQFLNORLNTDYLARVNAELRGL 120
Db      61 LKLVGSLIGKRILSELWGLIFPSGSTNLMODILRETEQFLNORLNTDYLARVNAELRGL 120
Qy      121 QANIREFOVDNFANPTONPVPLSTSSVNTMOQLFLNRLPFOIOGYOLLPLPFAQA 180
Db      121 QANIREFOVDNFANPTONPVPLSTSSVNTMOQLFLNRLPFOIOGYOLLPLPFAQA 180

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QY 181 ANHLSFRDVLNADENWISAAATLRTYQNYLAKNTTEYSYCLNTYQTPARGLNTRLD 240
DB 181 ANHLSFRDVLNADENWISAAATLRTYQNYLAKNTTEYSYCLNTYQTPARGLNTRLD 240
QY 241 MLBERTYMFANFEYYSIMSLEFKYOSILVSSGANLYASGGSPQOTOSFTSODWPELYSLF 300
DB 241 MLBERTYMFANFEYYSIMSLEFKYOSILVSSGANLYASGGSPQOTOSFTSODWPELYSLF 300
QY 301 QVNSNYVLANGSGARLLTOTPNIGLPGTTTHALLARVNSGCVSSGDIGAV-ENONE 359
DB 301 QVNSNYVLANGSGARLLTOTPNIGLPGTTTHALLARVNSGCVSSGDIGAV-ENONE 359
QY 301 QVNSNYVLANGSGARLLTOTPNIGLPGTTTHALLARVNSGCVSSGDIGAV-ENONE 359
DB 301 QVNSNYVLANGSGARLLTOTPNIGLPGTTTHALLARVNSGCVSSGDIGAV-ENONE 359
QY 360 SCSTFELPLLTPEFVSMIDSGDRGVNVTVMQTESPESTGLRCGAFARAGNSNYPD 419
DB 360 SCSTFELPLLTPEFVSMIDSGDRGVNVTVMQTESPESTGLRCGAFARAGNSNYPD 419
QY 361 NCSTVLEPLSTPEFVSMIDSGDRGVNVTVMQTESPESTGLRCGAFARAGNSNYPD 420
DB 361 NCSTVLEPLSTPEFVSMIDSGDRGVNVTVMQTESPESTGLRCGAFARAGNSNYPD 420
QY 420 YFIRNIGVPLVVRNEDLRPLAHNEIRNIESPSGTPGGLAAVMSVHRKKNIIYAHEN 479
DB 420 YFIRNIGVPLVVRNEDLRPLAHNEIRNIESPSGTPGGLAAVMSVHRKKNIIYAHEN 479
QY 421 YFIRNIGVPLVVRNEDLRPLAHNEIRNIESPSGTPGGLAAVMSVHRKKNIIYAHEN 480
DB 421 YFIRNIGVPLVVRNEDLRPLAHNEIRNIESPSGTPGGLAAVMSVHRKKNIIYAHEN 480
QY 480 GTMHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDGLFEQSNITRAYTLKNG 539
DB 480 GTMHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDGLFEQSNITRAYTLKNG 539
QY 481 GTMHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDGLFEQSNITRAYTLKNG 540
DB 481 GTMHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDGLFEQSNITRAYTLKNG 540
QY 540 NSYNLYLRVSS 550
DB 540 NSYNLYLRVSS 550
QY 541 NSYNLYLRVSS 551
DB 541 NSYNLYLRVSS 551

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RESULT 6

08KNY2 PRELIMINARY; PRT; 1231 AA.

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ID 08KNY2; PRELIMINARY; PRT; 1231 AA.
AC 08KNY2; 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE CRYI11.
GN CRYI11.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CX NCBI_TaxId=1428;
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=834;
RA Isaakova I.A., Isaakov Y.B., Rymar' S.E., Yarovoi S.V.;
RT "Cloning of a novel Bacillus thuringiensis cryI11 gene for
insecticidal crystal protein."
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY138457; AAM93496.1; -.
DR InterPro: IPR001178; Endotoxin.
DR InterPro: IPR005638; endotoxin_C.
DR InterPro: IPR005639; endotoxin_N.
DR Pfam: PF00555; endotoxin_1.
DR Pfam: PF03944; endotoxin_C; 1.
DR Pfam: PF03945; endotoxin_N; 1.
SQ SEQUENCE 1231 AA; 139765 MW; C9F2848A9297EAD0 CRC64;

```

Query Match

9.9%; Score 328.5; DB 2; Length 1231;
Best Local Similarity 23.3%; Pred. No. 2, 1e-13;
Matches 155; Conservative 101; Mismatches 249; Indels 161; Gaps 29;

```

QY 52 PIVGVTSFLKKVGLIGKRIISLWGLIFPSGSTNLMODILREHGFQINORLNTDTLA 111
DB 73 PFAQGLASFSFLVQ-----ELM-----PSG-RDPWEIFLEHVEQLIKQVNTENTRN 118
QY 112 RNVAELLEGQANIREFNOQVDNFIANTQNPVPLSITSVNTMOQ-LFNRLLPQFVQVQ 170
DB 119 TAAALEGGRGRYRQQALETWLDNRNARSRIILERVVALELDITTAFLPRINNEE 178
QY 171 LLLPLPFAQANHLISFRDVLNADENWISAAATLRTYQNYLAKNTTEYSYCLNTYQTA 230
DB 179 VPLIMVYAQANHLILRLDASLFGSEWGMASDVNOYQEQIRTYEISNHCQMYNTG 238

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QY 231 FRGL-NTRIHML-----EFTYMFANFEYYSIMSLEFKYOSILVSSGANL-----YASGSP 282
DB 239 LNNLNGTASWLRVNOQFRDLTLGLDLVALPSPYDTETPEYISQQLREIYTDPIGR 298
QY 283 QCTQS-FTSQW-----PFLYSIFQVNSNY-----LNGPSG 313
DB 299 TNAPSGFASLWENNNAAPSEALIEAATIRPHLLDPPEBLITVYSSSWMSTQHMNYWVG 358
QY 314 ARLTQFPNIGLPGTTTHALLARVNSGCVSSGDIGAVNONFSCSTFELPLLTPEV 373
DB 359 HRL--NFRPIGTLNIST-----QGLTNYSINFTLOFT 391
QY 374 RSWLDSGSDRGV-----TVTN-----NOTESPESTGLRCGAFARAGNSNYPDIFRNS 426
DB 392 SRDVRFTESNAGNTLLETPYNGVMDRFNINQNI-----YENGATVYQPY-----Q 441
QY 427 GVLVVRNEDLRPLAHNEIRNIESPS-----GTPGGLAAVMSVHRKKNIIYAHEN 467
DB 442 GVGIGLQFDETELPETTERPNYESHRLSHIGLIGTLAPAPYSWTHRSADRTNITIG 501
QY 468 -NRKNIIYAHEN-----NGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDGL 522
DB 502 PNRITQIPAVKGRFLFNGSVI--SGPGFTGGDVRLNRNNQNIQRGYI-----EV 550
QY 523 RFQSNITRAYTLKNGNSYNLYLRVSSIGNSTIRVYI-NGRVTASVNTVTTNDCVND 581
DB 551 PIQFTSTSTRYKVR-----VRYASVTSIELNVMNGSSIFNTIIPATASLDLQOS 601
QY 582 NGARPLDIN-----MGNVVA-----SDVTNVPD-----INVTENGSTQPEL-----NFI 621
DB 602 GDFGYEINNATSAATGNIGANFSAVAEYIDRFEFIVTATBAYDIERAOKAVNA 661
QY 622 MEVPEVN 627
DB 662 LFTSTN 667

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RESULT 7

093N5 PRELIMINARY; PRT; 719 AA.

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ID 093N5; PRELIMINARY; PRT; 719 AA.
AC 093N5; 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE CRYIA.
GN CRYIA.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CX NCBI_TaxId=1428;
RN RN
RP SEQUENCE FROM N.A.
RA Song F., Zhang J., Gu A., Huang D., Li G.;
RT "A novel CryIIa endotoxin."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF373207; AAK66742.1; -.
DR InterPro: IPR001178; Endotoxin.
DR InterPro: IPR005639; endotoxin_C.
DR InterPro: IPR005638; endotoxin_N.
DR Pfam: PF00555; endotoxin_1.
DR Pfam: PF03944; endotoxin_C; 1.
DR Pfam: PF03945; endotoxin_N; 1.
SQ SEQUENCE 719 AA; 81225 MW; C629DF2C44827241 CRC64;

```

Query Match

9.9%; Score 327.5; DB 2; Length 719;
Best Local Similarity 22.8%; Pred. No. 1, 1e-13;
Matches 162; Conservative 103; Mismatches 271; Indels 173; Gaps 32;

```

QY 21 HDPSPFEK-----SLDTTRKEK-MEMKRTD-----SLY--VAP----- 52
DB 9 HOSFSSNAKYDKJSTSLKNETDIELONINHDCLMSEIENVPPFASATITOTGIGAG 68
QY 53 -IVGVTSFLKKVGLIGKRIISLWGLIFPSGSTNLMODILREHGFQINORLNTDTLA 111
DB 53 -IVGVTSFLKKVGLIGKRIISLWGLIFPSGSTNLMODILREHGFQINORLNTDTLA 111

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Db      69 KILGTLGVPPAGVAVSLY-SFILGELM-----PKGK-NQWELFMEHVEEIIINOKISTYARN 122
QY      112 RVNALEGLQANIREFNOVDNFIPTQNPVLSIT-SSVNTMOQLFNRIPORVQGY 170
Db      123 KALTDLKGDLALAVHDSLESVWGNRRNTRASVKSQYIALBELFVOKLSPAVSGE 182
QY      171 LLLPLPFAQANMLSFIRDVVLANDEGISAATLTFTYQNYLKNYTESNYCINTYQTA 230
Db      183 VLLPFIYAQANMLHLKLDASIFGKESGLSSSEISTFYNRQVERAGDSDHCWKYSTG 242
QY      231 FRGL-NTRLHDMU--EFTYVFLNFEVSIWGLFYQSLVSSGANU-----YASGSGP 282
Db      243 LNNLRGTNAESWVRVYQFRDMTLMVLDLVALPSPYDQWPIKTTAQLTREYTDALGT 302
QY      283 QQTQ-SFTSQDW-----PFL-----YSLFQVNSN-YVINGFSG 313
Db      303 VHPHSFTSTTYWNNNAPSFAIEAAVRNPHLDLFLBOVTIYSLSRMSNTQYNNMMWG 362
QY      314 ARLTQTPENIGLPGTTTHALLAARVNVSGVSGDIGAVNQNFSCGTEPLPPLLTPEV 373
Db      363 HKL--EFTTIGTTLNIST-----QGSTNTSINPVLTPFT 394
QY      374 RSWLDSGSDRGVTVY-----NMQ--TESPESTLGLRCGAFTRAGNSNTPPD 419
Db      395 SRDVRTESLAGNLFLTPVNGVRVDFFHKFVTHPIAS-----DNFYYPG 441
QY      420 YFIRNISGVPLVARNEDLRPLHNEIRNIESPGTGGGLAAVWVYHNRKNKIYA-VHE 478
Db      442 Y-----AGIGTQLODSENELPPEATGQPNYESYSHLSHG--LISASHKALVYSWTHR 494
QY      479 NGTMHILAPEDYGTISPIHATQV-----NNQRTFISEKFG-NOGDSLRFGSNTTA 531
Db      495 SA-----DRTN-TIEPNSITQIPLVKAFLSSGAAVRGFTGGDILR--RTNVTG 543
QY      532 RYTLRNGN-----SYNLVLRVSLGNSITRTVINGRVYTAASVNTTNNQDNGARF 586
Db      544 FEDIRVNIKPPAQRVIRIRYASTDLOFHTSINKKAINOGNSATMNR-----GSD 596
QY      587 LDINMGVVASDNTVPLDINVT-----FNSGTQFELNMIMFVPTNL 628
Db      597 LDYKTRTVGFTTPPSFLDVQSTFTIGAMNFSNGEYIIRLIEFVPEV 645

RESULT 8
ID 085796 PRELIMINARY; PRT; 719 AA.
AC 085796;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Insecticidal protein.
GN CRYV101.
OS Bacillus thuringiensis (subsp. kurstaki).
OC Plasmid large plasmid.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=SI01;
RC Zhong O., Deng R., Long O., Yuan M., Pang Y., Wang X.,
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF076953; AAC26910.1; -.
DR HSP; F02965; ICY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF00555; endotoxin_1.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
KW Plasmid.
SQ
SEQUENCE 719 AA; 81230 MW; 42745D478359BBA7 CRC64;
Query Match 9.8%; Score 325.5; DB 2; length 719;

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Best Local Similarity 22.7%; Pred. No. 1.6e-13;
Matches 161; Conservative 103; Mismatches 272; Indels 173; Gaps 32;

QY      21 HDPPSEERK-----SDTIRKEM-MEMKRTD-----SLV--VAP----- 52
Db      9 HOSFSSNAVKIDSTDSLAKNETDIELQINNHEDCLAKSEVENPEPVASVSTIGIGIAG 68
QY      53 -IYQVSSFLKQVSLGRIISLMLGLIPSGSTNMODLIRETQFLNORLNTDTLA 111
Db      69 KILGTLGVPPAGVAVSLY-SFILGELM-----PKGK-NQWELFMEHVEEIIINOKISTYARN 122
QY      112 RVNALEGLQANIREFNOVDNFIPTQNPVLSIT-SSVNTMOQLFNRIPORVQGY 170
Db      123 KALTDLKGDLALAVHDSLESVWGNRRNTRASVKSQYIALBELFVOKLSPAVSGE 182
QY      171 LLLPLPFAQANMLSFIRDVVLANDEGISAATLTFTYQNYLKNYTESNYCINTYQTA 230
Db      183 VLLPFIYAQANMLHLKLDASIFGKESGLSSSEISTFYNRQVERAGDSDHCWKYSTG 242
QY      231 FRGL-NTRLHDMU--EFTYVFLNFEVSIWGLFYQSLVSSGANU-----YASGSGP 282
Db      243 LNNLRGTNAESWVRVYQFRDMTLMVLDLVALPSPYDQWPIKTTAQLTREYTDALGT 302
QY      283 QQTQ-SFTSQDW-----PFL-----YSLFQVNSN-YVINGFSG 313
Db      303 VHPHSFTSTTYWNNNAPSFAIEAAVRNPHLDLFLBOVTIYSLSRMSNTQYNNMMWG 362
QY      314 ARLTQTPENIGLPGTTTHALLAARVNVSGVSGDIGAVNQNFSCGTEPLPPLLTPEV 373
Db      363 HKL--EFTTIGTTLNIST-----QGSTNTSINPVLTPFT 394
QY      374 RSWLDSGSDRGVTVY-----NMQ--TESPESTLGLRCGAFTRAGNSNTPPD 419
Db      395 SRDVRTESLAGNLFLTPVNGVRVDFFHKFVTHPIAS-----DNFYYPG 441
QY      420 YFIRNISGVPLVARNEDLRPLHNEIRNIESPGTGGGLAAVWVYHNRKNKIYA-VHE 478
Db      442 Y-----AGIGTQLODSENELPPEATGQPNYESYSHLSHG--LISASHKALVYSWTHR 494
QY      479 NGTMHILAPEDYGTISPIHATQV-----NNQRTFISEKFG-NOGDSLRFGSNTTA 531
Db      495 SA-----DRTN-TIEPNSITQIPLVKAFLSSGAAVRGFTGGDILR--RTNVTG 543
QY      532 RYTLRNGN-----GNSYNLVLRVSLGNSITRTVINGRVYTAASVNTTNNQDNGARF 586
Db      544 FEDIRVNIKPPAQRVIRIRYASTDLOFHTSINKKAINOGNSATMNR-----GSD 596
QY      587 LDINMGVVASDNTVPLDINVT-----FNSGTQFELNMIMFVPTNL 628
Db      597 LDYKTRTVGFTTPPSFLDVQSTFTIGAMNFSNGEYIIRLIEFVPEV 645

RESULT 9
ID 08K761 PRELIMINARY; PRT; 719 AA.
AC 08K761;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Cry.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Porcar M., Martinez C., Caballero P.,
RT "Identification and characterization of a novel cry gene from Bacillus
RL thuringiensis.".
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF278797; AAM73516.1; -.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.

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DR Pfam: PF00555; endotoxin; 1.
 DR Pfam: PF03944; endotoxin C; 1.
 DR Pfam: PF03945; endotoxin N; 1.
 DR SEQUENCE 719 AA; 80984 MW; 84F1287246264473 CRC64;

Query Match 9.8%; Score 323.5; DB 2; Length 719;
 Best Local Similarity 22.7%; Pred. No. 2.1e-13;
 Matches 160; Conservative 11; Mismatches 269; Indels 165; Gaps 34;

21 HDPEFEHK---SLDTRKEM-MEMKRTDH-----SLY-VAP-----52
 9 HQSFSSNAKVDKISTDSIKNETDIELQNIHBDCLIKSEYNEVPEVSASTIQTGISIAG 68
 53 -IVGTUSFLKKGSLIGKRIISLSELMGLIFSGSGSTNMODLRETEOPINQRLNTDTLA 111
 69 KILGTGLVPPAGVASTLY-SFLIGELM-----PKKG-NQMEIFMEHVEELINQKSTAYRN 122
 112 RVNALEKGLQANIRENQOVNPLPTQNPVLSIT-SSVNTMOQLFLARLPQRYVQYQ 170
 123 KALFDLGLDALAVYHESLESVGNKNTKRRASVVKQYIALMFWKLSFSAVSGEE 182
 171 LLLPLFAQANMHSPIRDVYLNADEMGISAATLRTYQNIKNYTYEYNYCINTYQTA 230
 183 VPLPIYAQANMHLILRLDASIRGKEMGLSSEISTFYNQVERAGDYSDHCVMYGTG 242
 231 FRGL-NTRLHDL-EEFTYFPLNVEYVSYSLFKQSL--VSSGANL---YAGS 280
 243 LNNLRGTNAESWVRVYQFQKDWLMLDLVLEP-SYDVLVYPIKTSQLTREYVTDAL 300
 281 GP-QQTQSFISQDM-----PFL-----YSLFOVNSN-YVLNGF 311
 301 GYVHPNNSFASFTTWNNNNAPSFTLESAYVRNHLIDPLEQVTIYSLSRWSQYQMMMW 360
 312 SGARLTQTPNIGLGTGTTTALLAARVYSGVSSGIGAVNQNFSCSTPLPLTP 371
 361 GGHRL--EFTIGMNTST-----QGSTNHSINPVTL 392
 372 FVRSWLDGSDRGGVTVT-----NMQ--TESFESTLGLRCGAFARQNSNYF 417
 393 FTSRDVYTESLGLMLFLTPVNGVPRVDFHMKFVTHPLAS-----DNFY 439
 418 PLYFRNLSGVPLVKNEDLRRLAYNEINHSPPGTGGLRAYVSVNRKNNTYA-V 476
 440 PGT-----AGTQQLDQSENELPPTTQQPVYSYHRLSHG--LISAHVYALVYSMT 492
 477 HENGTMHLAEDYTGFTISPIHATQV-----NNOTRTFISEKFG-NQGDLSRFGQSYT 529
 493 HNSA-----DRTN-TIEPNSITQILPVKAFVLSGAAVVRGPGFTGDILR-RNT 541
 530 TARTYLKNGN-----SYNLVLRVSLGNSITRVTLNGRVYASVNTTENDGVANDGA 584
 542 GTFGDIRVNIAPPQARYRIRIKYASTIDQFHTSINGKAINQGFSAITNMR-GEOLDYK 600
 585 RFLDINMGVVASDNTVPLDINV-TENSGTQFLKNIWVPTNL 628
 601 TFRVGTTPPSFSDVQSTFTIGAMNFSGNEVYIDRIEVEV 645

RESULT 10
 Q9F0P8 PRELIMINARY; PRT; 719 AA.

AC Q9F0P8;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, last annotation update)
 DE CRYII.
 GN CRYII.
 OS Bacillus thuringiensis.
 OC Bacillales; Bacillaceae; Bacillus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN (1)
 RP SEQUENCE FROM N.A.

RC STRAIN=PRC007;
 RA Song F., Zhang J., Huang D., Li G.
 RT "The Cloning of a novel cryII gene from Bacillus thuringiensis
 strain..."
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF211190; AA043526.1; --
 DR HSSP; P02965; IC1Y.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; endotoxin_C.
 DR InterPro; IPR005639; endotoxin_N.
 DR Pfam; PF00555; endotoxin; 1.
 DR Pfam; PF03944; endotoxin C; 1.
 DR Pfam; PF03945; endotoxin N; 1.
 KW PfamId.
 SEQUENCE 719 AA; 81025 MW; 7E17481922C435E6 CRC64;

Query Match 9.6%; Score 317.5; DB 2; Length 719;
 Best Local Similarity 22.7%; Pred. No. 5.4e-13;
 Matches 154; Conservative 113; Mismatches 273; Indels 139; Gaps 32;

19 VADPR--SPHKSLDTRKEMEMKRTDHSLYVA-PIYGVVSFLKKGSLIGKRIIS 75
 37 INHEDFLKMSHESID-----PPVASTIQTGIGAKILGTGVPPAGQIASLY-SFLIG 91
 76 ELWGLIFSGSTNLMQDILRETEQFLNQLNTDTLARVNALEKGLQANIRENQOVNPL 135
 92 ELW-----PKGSKQ-WEIFMEHVEELIDKISTYARNIALDLKGLDALAVYHESLESW 146
 136 NPQNQVPLSIT-SSVNTMOQLFLARLPQRYVQYQQLLLPLFAQANMHSPIRDVYLN 194
 147 KKNMBAKTSVVKQYIALMLFLVQQLPSFAVSGEVPPLPIYAQANMHLILRLDASV 206
 195 ADEMGISAATLTATYQNIKNYTYEYNYCINTYQTAARG-NTRLHDL-EEFTYFPL 250
 207 GKENGJNSQISTFQNRQVETSDSDHCVMYGTGIANLRGTNAESWVRVYQFQKDWL 266
 251 NVEFYVSYSLFKQSL--VSSGANL---YAGSGP-QQTQSFISQDM-----293
 267 MVLDLALFP-SYDVLVYPIKTSQLTREYVTDALGVHPNNSFASFTTWNNNNAPSFS 324
 294 -----PFL-----YSLFOVNSN-YVLNGFSGARLTQTPNIGLPGTTTHAL 335
 325 TESAVRNPPLIDPLEQVTIYSLSRWSQYQMMWGHIL-EEFTIGVYLTNT-----378
 336 LAARVYSGVSSGIGAVNQNFSCSTPLPLTPPYRSWLDGSDRGGVTVT-----390
 379 -----QGSTNHSINPVTLPTFRSDVYTESLGLMLFLTPVNGVPRVDFHMKF 416
 391 -----NMQTESFESTLGLRCGAFARQNSNYFPDYFIRNISGVPLVKNEDLRRL 443
 417 GVPVDFHMKF--ATLPASDNF-----YVLGY-----AGVTQQLDSENELPPT 460
 444 NEIRNISPSTPGGLRAYVSVNRKNNTYA-VHENGTMHLAEDYTGFTISPIHATQ 502
 461 TQQPVYSYHRLSHG--LISAHVYALVYSMTRSA-----DRTN-TIEPNSITQ 509
 503 V-----NNOTRTFISEKFG-NQGDLSRFGQSYT-----SYNLVLRVSS 550
 510 IFLYKAPNLSGAAVVRGPGFTGDILR-RNTGTGFDIRVININPPQARYRIRYAS 567
 551 LGNSTIRVTNGRVYASVNTTNDGVANDGARFLDINMGVVASDNTVPLDINV-T 609
 568 TTDLQFHTSINGKAINQGFSAITNMR-GEOLDYKTFRTVGTTPPSFSDVQSTFTIGAMN 626
 610 FNSGTQFLKNIWVPTNL 628
 627 FSSGNEVYIDRIEVEV 645

RESULT 11
 Q9S5V8 PRELIMINARY; PRT; 1180 AA.

AC Q9S5V8;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, last annotation update)
 DE CRYII.
 GN CRYII.
 OS Bacillus thuringiensis.
 OC Bacillales; Bacillaceae; Bacillus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN (1)
 RP SEQUENCE FROM N.A.

DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
 DE BT8441 crystal protein (Crystal protein CryIA).
 GN BT8441.
 OS *Bacillus thuringiensis*, and
 OC *Bacillus thuringiensis* (subsp. sotto).
 OC *Bacteria*; *Firmicutes*; *Bacillales*; *Bacillaceae*; *Bacillus*.
 OX NCBI Taxid=1428, 29340;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=B. *thuringiensis*; STRAIN=T84A1;
 RA Ogo M., Yamada S., Kobayashi Y., Shibata J., Nagamatsu Y.;
 RT "Nucleotide Sequence of the Lepidoptera-toxic Protein Gene of *Bacillus thuringiensis* subsp. *dendrolimus* T84A1.";
 RL J. Pac. Appl. Biol. Sci. Hiroshima Univ. 29:95-107 (1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=B. *thuringiensis*; STRAIN=T84A1;
 RA Nagamatsu Y., Imai Y., Hatanaka C., Funatsu G., Hayashi K.;
 RT "A Toxic Fragment from the Entomocidal Crystal Protein of *Bacillus thuringiensis*.";
 RL Agric. Biol. Chem. 48:611-619 (1984).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=B. *thuringiensis* (subsp. sotto);
 RA Zhong W.F., Cai P.Z., Yan W.Z., Zhang X.X., Xiang Y.W.;
 RT "A cryIA gene cloned from *Bacillus thuringiensis* serovar sotto.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB026261; BAA77213.1.
 DR EMBL; AF510713; AAM44305.1.
 DR HSSP; P02965; 1C1Y.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; endotoxin_C.
 DR InterPro; IPR005639; endotoxin_N.
 DR Pfam; PF00555; endotoxin_1.
 DR Pfam; PF03944; endotoxin_C.1.
 DR Pfam; PF03945; endotoxin_N.1.
 SQ SEQUENCE 1180 AA; 133489 MW; 1199E4A6D1DC62D CRC64;
 Query Match 8.5%; Score 280.5; DB 2; Length 1180;
 Best Local Similarity 21.7%; Pred. No. 3.4e-10;
 Matches 152; Conservative 104; Mismatches 272; Indels 173; Gaps 29;
 Oy 6 NNGRTTICDAVAVVAHDPFSEHKSIDTIRKEMMERK--DHSLYVAPIVGVSSFLK 63
 Db 3 NNNINEICIPNCIS-----NPEVAVUGGERIEGYTPIDISL-----SLTQFLLS 48
 Oy 64 K-----VGLIGKRLISLWKLIFPGSGTNLMODLRETQFOLNORLNDTLAVNMLEBG 119
 Db 49 EAVPAGAFVLD--LVDTIMGIFGPS---QMDAFLVQIQLLNQRIEEFANQAIISRLGG 102
 Oy 120 LG-----ANIREFNOVDNFTLPTQNPVLSTSVTMQQLFLRQPOVQOYL 172
 Db 103 LSNLYQIYAESFREWE-----ADPTNALREERKQFQDMASALTITLPLFAVQVQVP 156
 Oy 173 LLELFAQANWHLSTFRDVLVLAADWGLSAATLPTQNTLKNYTTESNYCINTYQTAAR 232
 Db 157 LLSYVQANLHLSVLRDVSFGQWGFDAATINSRYNDLRLIGNTVDAVAVWYTGLE 216
 Oy 233 ---GLNTRLDML--EFTVWFLNVEPVYSLSLFYQSLVSSGANLYASGSGQOQO 286
 Db 217 RVMGPDNR--DWRYNQFRELITLVDIVALPS-----NDSRRPRTV 260
 Oy 287 SETSQDWPFYLSLFQVNSNYVUNGSGA-----RLTQTF--PIIGLPEPTTTALLAA 338
 Db 261 SGLTR-----ELYNPLVLENFDSFGMAQRLEONIRQPHLMDIINRITTYDVHR 311

Oy 339 RVNYSG--VSSGIDGAFNPNESCSTF-----LPELITP----- 371
 Db 312 GPNWSSHQITLSPVGE-----FSGEFAPPLFGNAGNAAPVILTGIGFTLSSPL 365
 Oy 372 FVRSMLDSGSDRGVAVTVMQTESFSTGLRCGAFARANSNSPPDFINISGVPLV 431
 Db 366 YRRIILSGPNNOLFVLDIGTESFASLTNLPSTIYQKGT-----VSLDVLIPQ 417
 Oy 432 VRNEDLRRLAH--NEINIESPSGTPGGLRANVSVHNRK--NNIYAVH-- 478
 Db 418 DNSVPPAGFSRLSHVTMLSQAGAVVTLRAPTFSMOHSABFNIIIPSSQITQIPLTK 477
 Oy 479 ---NGMILHAPEDYTGFTISPIHATQVNNQRTFRISKFGNQGDSLRFEQNTARY 533
 Db 478 STNLGSGTSVXGP-----GFT-----GDLIR--RTSPQOIS 508
 Oy 534 TLGN-----GNSVULYKRPSSIGNSTIRVTVNGRVYASVNTTNDGVNDGARPLD 588
 Db 509 TLKVNITAPLSQRTKVRIRIRASTTNLQFHTSIDRPTNQGNSFATWS--GSLQSGSFT 567
 Oy 589 INNGNVASDNTNPLDINV--TENSQTQPELMNIMFVPTNL 628
 Db 568 VGFTTFPNSGSSVFTLSAHVFNSGNEVYIDRIEFPVPAEV 608
 RESULT 12
 ID 09S603 PRELIMINARY; PRT; 645 AA.
 AC 09S603
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
 DE Delta-endotoxin (Fragment).
 OS *Bacillus thuringiensis*.
 OC *Bacteria*; *Firmicutes*; *Bacillales*; *Bacillaceae*; *Bacillus*.
 OX NCBI Taxid=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=serovar japonensis type;
 RA MEDLINE=99025985; PubMed=9806979;
 RA Maeda N., Ohba M.;
 RT "Assignment of delta-endotoxin genes of the four lepidoptera-specific *Bacillus thuringiensis* strains that produce spherical parasporal inclusions.";
 RL Curr. Microbiol. 37:408-411 (1998).
 DR EMBL; AF042733; AAB97923.1.
 DR HSSP; P07130; 1DLC.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; endotoxin_C.
 DR InterPro; IPR005639; endotoxin_N.
 DR Pfam; PF00555; endotoxin_1.
 DR Pfam; PF03944; endotoxin_C.1.
 DR Pfam; PF03945; endotoxin_N.1.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 645 AA; 72967 MW; 143BE1312B89CE3 CRC64;
 Query Match 8.4%; Score 279.5; DB 2; Length 645;
 Best Local Similarity 22.1%; Pred. No. 1.7e-10;
 Matches 149; Conservative 94; Mismatches 276; Indels 155; Gaps 28;
 Oy 13 CDAYNVADHPSPFSEHKSIDTIRKEMMERKIDHSLYVAPIV--TVSSFLKKVSGSLI 69
 Db 4 CPADVDVKTPLTDDNAGLQNM--NYKEYLQYGGDYDPLINPNISVSGKDVIGVGINI 61
 Oy 70 GKRLS-----ELMGLIFPGSGTNLMODLRETQFOLNORLNDTLARVN 114
 Db 62 VGRILSFGFPSSQWVTVTYLLNSLWPDENSVMQAFERREBELIDOKSEAVKRAL 121
 Oy 115 AEEGAGQANIREFNOVDNFTLPTQNPVLSTSVTMQQLFLRQF--RVGQYQ 170
 Db 122 DDLTGLOVYNNLYEALDSWLNRPNGARASLVSGRFNIIISLFTQPMPSFGSGGQNYA 181

QY 171 LLLLEPFAQAMNHLSFRDVVNLADENGLSATLRTYQNYLNTTEYSNYCINTYQTA 230
 DB 182 TLLPFAQAMNHLSFRDVVNLADENGLSATLRTYQNYLNTTEYSNYCINTYQTA 241
 QY 231 FRGL-NTLHMLLEFRY---MFLNFEYVLSLFLKQSLVSSGAMLVSSGSGPQTA 286
 DB 242 LAELRGTAAESWFKNQYREMTLTLMDLV---ALPEYVNL---ROYDGTNPQTR 292
 QY 287 SF-----TSQ---DW-----PFLY---SLFOVNSN 305
 DB 293 EYVTDPLADPLEQPTTQCGSWYINPAFRNHLNPSVLNSLRPHLERLSLQILVN 352
 QY 306 YVING--FSGARLTQTFPNIGLPGTTTHALLARVNSGSGDGAIVNQFSGST 363
 DB 353 YQVNGSAMRGSVRVRYHSSIT--QEKSYGLSDPGANLNNQNDIYQIISQ---VSN 407
 QY 364 FLPLPLTFP---VRSWLDGSDRG---GVNTVNMQTSFESTGLRCAAFTRG 412
 DB 408 FASPVGSSYSVWDTNPNVLSGVSIGYTOOGIPAVCLQORNSDELPSLMEGDIIRN 467
 QY 413 NS---NYFPDY-FIRNIGSVPLV-----RNEDLRPLHYNEIRNI-----ES 451
 DB 468 YSHRLSHITQYRFQATQSSPSYSANLPTCWTNRDVLNNTITANQITQPLKAYEL 527
 QY 452 PSG-----TPGGLRNVSVNRKNNIYAVHENGTMHIALPEDYIGF 493
 DB 528 SSGATVYKGPFTGVDVIRNTGFGALIRVSTGFLTORVRIR---FRYASTIDPDF 583
 QY 494 TISPLHATQVNN--QRTTISKXNGQSDSLREQSNLTARTLRGNSYNYLARSLS 551
 DB 584 VTR--GGTTNNFRFRITM-----NRQESRIE-SYRIVETTPFNFGSDIIRTSIQ 634
 QY 552 GNSITRVINGRYV 565
 DB 635 GUGS-----NGEVY 643

RESULT 13
 Q93NMS PRELIMINARY; PRT; 1228 AA.
 AC Q93NMS; 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
 DE CRY1BA.
 GN CRY1BA.
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang J., Song F., Huang D.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A8368257; AAK63251.1; -
 DR InterPro: IPR001178; Endotoxin_C.
 DR InterPro: IPR005638; Endotoxin_C.
 DR InterPro: IPR005639; Endotoxin_N.
 DR Pfam: PF00555; endotoxin_1.
 DR Pfam: PF03944; endotoxin_C_1.
 DR Pfam: PF03945; endotoxin_N_1.
 SQ SEQUENCE 1228 AA; 13966 MW; E86D9842341F439 CRC64;

Query Match 8.4%; Score 278.5; DB 2; Length 1228;
 Best Local Similarity 22.1%; Pred. No. 4.8e-10;
 Matches 152; Conservative 100; Mismatches 228; Indels 209; Gaps 33;

DB 52 PIVGTASSFLKKGSLIGRIISLWGLIFPSSGTNIMODLRETEQNLQNTDTLA 111
 DB 68 PFGAOLASFYSFVVG-----ELM---PRG-RDQWELFEHVEQLNQITENARN 113
 QY 112 RVNALEGGQANIRENQOVNPLNPTONPVLSITSSVNTMOOL-FINRLPQRFVQGY 170
 DB 114 TALARKLQGLDSFRAYQGLSDLEWENRNDARSRVLTLYQYALTEPLNAMPFAIRNOE 173

QY 171 LLLLEPFAQAMNHLSFRDVVNLADENGLSATLRTYQNYLNTTEYSNYCINTYQTA 229
 DB 174 VPLLNVTAQAMNHLSFRDVVNLADENGLSATLRTYQNYLNTTEYSNYCINTYQTA 233
 QY 230 --AFRGLN---TRLHMLLEFRY---MFLNFEYVLSLFLKQSLVSSGAMLVSSGSGPQTA 279
 DB 234 LNSLGTAAASWRYN---QFRRLTLGLVLDVALFSPYDTRITYPINTSQAOLREYITDA 290
 QY 280 SGPQQTQSGSDW-----PFL-----YSLFOVNSNYV---LNGF 311
 DB 291 IGATGV-NMAMWYNNMNAAPSALTAARSPHLDFLEQTLIFSASSRWSTRTMYTW 349
 QY 312 SGARLTQTFPNIGLPGTTTHALLARVNSGSGDGAIVNQFSGST 355
 DB 350 RG-RTIQSRPIGGGL--NTSTGATNTSINPVLTRASADVRTESYAGVLWG----- 400
 QY 356 NQFSGSTFLPLTLTPFVRSWLDGSDRGVNTV---TNMOTESFESTGLRCAAFTR 411
 DB 401 -----IYLEPI-----HGVPVTRNFTNPON-----ISDR 425
 QY 412 GNSNTPEDYFRNIGSVPLVWNEDELREPLHYNEINIESPGTQGLRANVSVNRKN 471
 DB 426 GTANVSQPY-----ESPGLOLQDSETELPETTRRYVESYHR---LSHGILLQSRVN 477
 QY 472 -NIYA-VHENGTMHIALPEDYIGFTISPLHATQVNNQRTTISKXNGQSDSLREQSNLT 529
 DB 478 VPYVSWTRSA-----DRIN-TIGPNRITQI---PMYKASLPGQTV----- 516
 QY 530 TARTYLRNG-NSNVLRLVRSLSGNSITRVING-----RVYASVAVNTTNNDO 578
 DB 517 ---VRGGFTGGLILRTNTGFGPILRVNGPILQRVIRGFASTVDFPFVSRGG 571
 QY 579 VINDGARFL-----DINMGNVV-----ASDNTNPLD--- 605
 DB 572 TVNNFRPLRTNNSGDEIKYGNFVRAPFTPTPTQIIDIIRTSIQGLSGGSEVYIDKIE 631
 QY 606 -INVTNRSQTEP-----NMIMFVTN 627
 DB 632 IIPVATFPAETDLERQAEVAVNALFTNTN 660

RESULT 14
 Q45740 PRELIMINARY; PRT; 381 AA.
 AC Q45740; 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
 DE Insecticidal crystal protein (CryI) (Fragment).
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EG6346; PubMed=2061280;
 RX MEDLINE=91286178; Jelen A., Gilbert M.P., Jany C.S., Johnson T.B.,
 RA Gawron-Burke C.;
 RT "Isolation and characterization of a novel insecticidal crystal
 protein gene from Bacillus thuringiensis subsp. aizawai.";
 RT J. Bacteriol. 173:3966-3976(1991).
 DR EMBL: M63897; AAK2349.1; -
 DR HSSP: P07130; IDC
 DR InterPro: IPR001178; Endotoxin.
 DR InterPro: IPR005639; Endotoxin_N.
 DR Pfam: PF00555; endotoxin_1.
 DR Pfam: PF03945; endotoxin_N_1.
 FT NON TER 381
 SQ SEQUENCE 381 AA; 42967 MW; DDAEF0D0504CB36C CRC64;

Query Match 8.4%; Score 277.5; DB 2; Length 381;
 Best Local Similarity 26.3%; Pred. No. 1.1e-10;

Matches 100; Conservative 66; Mismatches 135; Indels 79; Gaps 19;

QY 21 HDPSEFEK-----SDTIRKEW-MEWKRTDH-----SLY-VA-P-----52
 Db 9 HOSFSSNAKYDKISTDLSLNKRETDIELQINIHEDCLISIEYENVEPVSASTOTGISTAG 68
 QY 53 -IVGVSSFLKKVGLSLQKRLISELWGLIFPGSGTNMODILRETEQFLNRLNTDTLA 111
 Db 69 KLTGLVPPAGQVAVSLY-SFLGELM---PFGK-NQWEIFMEHVEIILNOKISTYARN 122
 QY 112 RVNABELQANIRENQVDNPLNTPQNPVLSIT-SSVNTMOQLFLNLPQPVQGY 170
 Db 123 KALYDLKGLGDLAVVHESLESWGNKNTFRASVYKQYALALMEVQKLESEFVSGEE 182
 QY 171 LLLPLFOAANHLSPFRDVLNADWGLSAATLRTYQNTLYKNYTERISNCTNYQTA 230
 Db 183 VPLPIYQANLHLHLKDSIFGKESGSSSEISTFYNNQVERADYSDHCVMYSTG 242
 QY 221 FRGL-NTRLHDL---EFFRYMFLNVEVYSIWSLFKYQSL--VSSGANL---YASGS 280
 Db 243 LNNLRGTNAESWVRVYQFRKDMTLMVLDVAF--SYDLVVPKITSQILREYVTDAT 300
 QY 281 GP--QOTQSFQSDW-----PFL-----YSLPQVSN-YVANGF 311
 Db 301 GYVHPNASSFASTTWTNNNAPSFRTISSAVVRNPHLLDPLQCVTITSLSRMSNTQYNNMW 360
 QY 312 SGARLTQTPNIGLPGTTT 331
 Db 361 GGHRL--EFFRTGGMLNTST 378

RESULT 15
 ID 045720 PRELIMINARY; PRT; 620 AA.
 AC 045720.
 DT 01-NOV-1996 (TEMBLrel. 01. Created)
 BT 01-NOV-1996 (TEMBLrel. 01. Last sequence update)
 DT 01-OCT-2002 (TEMBLrel. 22. Last annotation update)
 DE CRYIA(A).
 GN CRYIA(A).
 OS Bacillus thuringiensis.
 EC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NRD-12;
 RX MEDLINE=9386467; PubMed=7657602;
 RA Maeson L., Lu Y.J., Mazza A., Brousseau R.,
 "The CRYIA(C) receptor purified from Manduca sexta displays multiple
 specificities.";
 J. Biol. Chem. 270:20309-20315(1995).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN-NRD-12;
 RX MEDLINE=95231292; PubMed=7715447;
 RA Maeson L., Mazza A., Gringorten L., Barnes D., Anellunas V.,
 Brousseau R.,
 "Specificity domain localization of Bacillus thuringiensis
 insecticidal toxins is highly dependent on the bioassay system.";
 Mol. Microbiol. 14:851-860(1994).
 RL EMBL; U43605; AAA86265.1; -
 DR HSSP; P02965; ICTY.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; endotoxin_C.
 DR InterPro; IPR005639; endotoxin_N.
 DR Pfam; PF00355; endotoxin_1.
 DR Pfam; PF03944; endotoxin_C; 1.
 DR Pfam; PF03945; endotoxin_N; 1.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 620 AA; 69428 MW; 4571A09E565E6DE CRC64;

Best Local Similarity 21.5%; Pred. No. 2.5e-10;
 Matches 151; Conservative 105; Mismatches 272; Indels 173; Gaps 29;

QY 6 NNGRTTICAYNVVHADDFEFKHSIDTIRKEWEMKRT--DHSLYVAIVGTUSFLK 63
 Db 3 NNPVINECIYVNCLS-----NPEVVGSGRIETGTPTDLSL-----SLTQFLS 48
 QY 64 K----VGSILGRILSELWGLIFPGSGTNMODILRETEQFLNRLNTDTLARVNAELG 119
 Db 49 EPPVGAQFVAG--LWDIIWGLFGRS---QMDAPLVOIEQLINRIEPPARNOAISLEG 102
 QY 120 LQ-----ANIRENQVDNPLNTPQNPVLSITSSVNTMOQLFLNLPQPVQGY 172
 Db 103 LSNLYQIYAESFEWE-----ADPTNPALEBKRIQPNUNSAITLTAIPLAVOYQVP 156
 QY 173 LLLPLFOAANHLSPFRDVLNADWGLSAATLRTYQNTLYKNYTERISNCTNYQTA 232
 Db 157 LLSVYQANLHLSLVDVSVFGQWGPDAATINSRYNDLTRIGNYTDVAVRWYNTGLE 216
 QY 233 --GLNTRLHDL---EFFRYMFLNVEVYSIWSLFKYQSLVSSGANLYASGSQPGQ 286
 Db 217 RVWGPDSR--DMVRYNQFRRLTLVLDVAFS-----NYDSRYPIRTY 260
 QY 287 SFTSQDWPEPLVSLQVNSVYVANGSGA-----RLTQTF--PNIGLPGTTTHALLAA 338
 Db 261 SOLTR-----EITNPELANPDSFRGMQRIKQNIROPHLMDLINSITTYDVHR 311
 QY 339 RVNYSQG--VSSGDIGAVRNQNFSGTF-----LPLLTP-----371
 Db 312 GFNYMSGHQTIVASPVG-----FSGPEFAFLPGNAGNAPVLVSLGIGIPRTLSPL 365
 QY 372 FVSWLDGSDRGCVNTVNTNMQTESFESTLGRCAFTARGSNTPFDYFIRNISGVPLV 431
 Db 366 YRIIILSGSPNNOELFVLDGTEFSPASLTNNLPSTTYRQGT-----VDSLDTVPPQ 417
 QY 432 VNEDLRPLHY--NRINISPSGTRGLRAYMVSVNRK---NNIYAVH-----478
 Db 418 DNSVPPRAGFHRSLHYTLQAGAVYTLRAPTFSMQHSLEFNIIIPSSQITQPLTK 477
 QY 479 ----NGTMHLAPEDYGTFTSPIHATQVNNQTRFISEKFGNQGSGLAFBSNTARY 533
 Db 478 STNLSSGTSVVKGP-----GFT-----GDIIR--RTSGQIS 508
 QY 534 TLRCN-----GNSYNYLAVSLANGSTIRVTINGRVYASVNTTNDGVNDGARFLD 588
 Db 509 TLKAVITLPLSQRYRRLRYASTNNLQPHTSIDGRPINQGFATWSS--GSLQSGSFRT 567
 QY 589 IMMGNVVASDNTVPLDINV--TPNSGTQPELNMVIFVPTNL 628
 Db 568 VGFTTPNFNSGSSVPTLSAHVFNSGMEVYIDRIEFPAAV 608

Search completed: August 14, 2003, 18:12:13
 Job time : 50 secs

Query Match 8.3%; Score 276.5; DB 2; Length 620;

